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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 06:56:33 ; Search time 2376.51 Seconds  
(without alignments)  
138.835 Million cell updates/sec

Title: US-09-800-629A-52  
Perfect score: 20  
Sequence: 1 tttctcagtcacagtttgt 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
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2: gb\_htg:\*  
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13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
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21: em\_ov:\*  
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29: em\_vl:\*  
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31: em\_htgo\_inv:\*  
32: em\_htgo\_hum:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_other:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	ARI36249 Sequence
2	20	100.0	24	6	A86923 Sequence 14
3	20	100.0	24	6	AR048335 Sequence
4	20	100.0	24	6	AR079226 Sequence
5	14.4	72.0	24	6	I28768 Sequence 3
6	14.4	72.0	24	6	I70526 Sequence 3
7	13.8	69.0	25	6	A22036 Oligonucleo
8	13.4	67.0	43	6	AX167229 Sequence
9	13.4	67.0	48	6	E15948 Primer. 7/1
10	13.2	66.0	34	6	A79313 Sequence 1
11	13.2	66.0	34	6	AR074516 Sequence
12	12.8	64.0	16	6	I72347 Sequence 3
13	12.8	64.0	17	6	I72348 Sequence 4
14	12.8	64.0	20	6	AX045082 Sequence
15	12.8	64.0	27	6	AX148237 Sequence
16	12.6	63.0	29	6	A35733 Synthetic o
17	12.6	63.0	29	6	AR007315 Sequence
18	12.6	63.0	29	6	I76376 Sequence 17
19	12.6	63.0	31	6	AR022300 Sequence
20	12.6	63.0	40	6	A35734 Synthetic o
21	12.6	63.0	41	6	A23270 mutagenic P
22	12.6	63.0	41	6	I52201 Sequence 1
23	12.4	62.0	25	6	A57414 Sequence 22
24	12.4	62.0	25	6	ARI31459 Sequence
25	12.4	62.0	27	6	A47990 Sequence 57
26	12.4	62.0	27	6	AX190998 Sequence
27	12.2	61.0	18	11	HSY19RAP1
28	12.2	61.0	24	6	AR051748 Sequence
29	12.2	61.0	24	6	I49693 Sequence 44
30	12.2	61.0	32	6	A87189 Sequence 1
31	12.2	61.0	33	6	AX000844 Sequence
32	12.2	61.0	42	6	AR021377 Sequence
33	12.2	61.0	42	6	AR042939 Sequence
34	12.2	61.0	42	6	I43928 Sequence 17
35	12.2	61.0	42	6	I62930 Sequence 25
36	12.2	61.0	42	6	I88683 Sequence 25
37	12	60.0	22	6	AX003318 Sequence
38	12	60.0	29	6	ARI49556 Sequence
39	12	60.0	41	6	AR077632 Sequence
40	12	60.0	41	6	AR077633 Sequence
41	12	60.0	41	6	AR077634 Sequence
42	12	60.0	44	6	AR034442 Sequence
43	12	60.0	44	6	AR070387 Sequence
44	12	60.0	45	6	AR099087 Sequence
45	12	60.0	45	6	AR099116 Sequence

ALIGNMENTS

RESULT 1  
ARI36249  
LOCUS ARI36249 20 bp DNA  
DEFINITION Sequence 52 from patent US 6136603.  
ACCESSION ARI36249  
VERSION ARI36249.1 GI:14476421  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.  
TITLE Antisense modulation of interleukin-5 signal transduction  
JOURNAL Patent: US 6136603-A 52 24-OCT-2000;  
FEATURES  
source Location/Qualifiers  
BASE COUNT 3 a 4 c 5 g 8 t  
ORIGIN

PAT

16-JUN-2001

*Power*

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttgt 20  
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Db 1 TTCTTCAGTCACAGTTGCT 20

## RESULT 2

LOCUS AR6923 24 bp DNA PAT 22-JAN-2000  
DEFINITION Sequence 14 from Patent WO9838306.  
ACCESSION AR6923  
VERSION AR6923.1 GI:6735707

KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dolganov, G.  
TITLE TRANSCRIPTS ENCODING IMMUNOMODULATORY POLYPEPTIDES  
JOURNAL Patent: WO 9838306-A 14 03-SEP-1998;  
GENELABS TECH INC (US)  
FEATURES Location/Qualifiers  
1..24

source

/organism="unidentified"  
/isolate="PRIMER IL5-1"  
/db\_xref="taxon:32644"

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ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttgt 20  
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Db 21 TTCTTCAGTCACAGTTGCT 2

## RESULT 3

LOCUS AR048335 24 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 14 from patent US 5821091.  
ACCESSION AR048335  
VERSION AR048335.1 GI:5970678

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dolganov, G.  
TITLE Method of identifying activated T-cells  
JOURNAL Patent: US 5821091-A 14 13-OCT-1998;  
FEATURES Location/Qualifiers  
1..24

source

BASE COUNT 9 a 7 c 4 g 4 t  
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttgt 20  
|||||  
Db 21 TTCTTCAGTCACAGTTGCT 2

## RESULT 4

LOCUS AR079226 24 bp DNA PAT 31-AUG-2000  
DEFINITION Sequence 14 from patent US 5965427.  
ACCESSION AR079226  
VERSION AR079226.1 GI:10005972

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dolganov, G. and Novikov, A.  
TITLE Human RAD50 gene and methods of use thereof  
JOURNAL Patent: US 5965427-A 14 12-OCT-1999;  
FEATURES Location/Qualifiers  
1..24

source

BASE COUNT 9 a 7 c 4 g 4 t  
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttgt 20  
|||||  
Db 21 TTCTTCAGTCACAGTTGCT 2

## RESULT 5

LOCUS I28768 24 bp DNA PAT 06-FEB-1997  
DEFINITION Sequence 3 from patent US 5573939.  
ACCESSION I28768  
VERSION I28768.1 GI:1819544

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS B.ang.vik,C.O., Eriksson,U. and Peterson,P.A.  
TITLE DNA encoding mammalian retinol binding protein receptor, and  
JOURNAL corresponding vectors and transformed cells  
FEATURES Patent: US 5573939-A 3 12-NOV-1996;  
source Location/Qualifiers  
1..24

BASE COUNT 9 a 5 c 7 g 3 t  
ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 24;  
Best Local Similarity 93.8%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 tcagtcacagttgt 20  
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Db 18 TCAGTCACAGTTGCT 3

## RESULT 6

LOCUS I70526 24 bp DNA PAT 03-APR-1998  
DEFINITION Sequence 3 from patent US 5679772.  
ACCESSION I70526  
VERSION I70526.1 GI:3006661

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS B.ang.vik,C.Olof, Eriksson,U. and Peterson,P.A.

TITLE Mammalian retinol-binding protein receptors  
JOURNAL Patent: US 5679772-A 3 21-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..24  
BASE COUNT 9 a 5 c 7 g 3 t  
ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 24;  
Best Local Similarity 93.8%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 tcagtcacagttgt 20  
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Db 18 TCAGTCCACAGTTGCT 3

RESULT 7  
LOCUS A22036. 25 bp DNA PAT 04-OCT-1994  
DEFINITION Oligonucleotide P4.  
ACCESSION A22036  
VERSION A22036.1 GI:641411  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Sonigo, P., Brechot, C. and Cournaud, V.  
TITLE Oligonucleotide sequences for amplification of type HIV-2 and siv  
retroviruses genomes and their application to in-vitro diagnostic  
of infections caused by these viruses  
JOURNAL Patent: EP 0404625-A 12 27-DEC-1990;  
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE  
MEDICALE (INSERM)  
FEATURES Location/Qualifiers  
source 1..25  
BASE COUNT 6 a 7 c 6 g 6 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 3.8e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 ctctcagtcacagttgt 19  
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Db 24 CTTAGTCACAGGTGG 8

RESULT 8  
LOCUS AX167229 43 bp DNA PAT 03-JUL-2001  
DEFINITION Sequence 8 from Patent WO0142463.  
ACCESSION AX167229  
VERSION AX167229.1 GI:14596696  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 43)  
AUTHORS Lu, J. and Wlitcher, D.R.  
TITLE Improving stability of flint through o-linked glycosylation  
JOURNAL Patent: WO 0142463-A 8 14-JUN-2001;  
ELI LILLY AND COMPANY (US)  
FEATURES Location/Qualifiers  
source 1..43  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligo primer"

BASE COUNT 13 a 11 c 14 g 5 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 43;  
Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcttcagtcacag 15  
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Db 9 TTCATCAGTCACACAG 23

RESULT 9  
LOCUS E15948. 48 bp DNA PAT 28-JUL-1999  
DEFINITION Primer.  
ACCESSION E15948  
VERSION E15948.1 GI:5710631  
KEYWORDS JP 1998113191-A/27.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Ishimura, M. and Nishigaki, T.  
TITLE HUMAN INTERFERON TAU VARIANT  
JOURNAL Patent: JP 1998113191-A 27 06-MAY-1998;  
SANKYO CO LTD  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1998113191-A/27  
PD 06-MAY-1998  
PF 20-AUG-1997 JP 1997223318  
PR 21-AUG-1996 JP 96P 219879  
PI ISHIMURA MASAKO, NISHIGAKI TAKASHI  
PC C12N15/09, A61K38/21, A61K38/21, C07H21/04, C07K14/555,  
PC C12N1/21,  
PC C12P21/02, (C12N1/21, C12R1:19), (C12P21/02, C12R1:19); CC  
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CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
FH key Location/Qualifiers  
FH

FEATURES source 1..48  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 7 a 15 c 14 g 12 t  
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 cagtcacagttgt 20  
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Db 40 CAGTCACAGCTGCT 26

RESULT 10  
LOCUS A79313 34 bp DNA PAT 20-OCT-1999  
DEFINITION Sequence 1 from Patent WO9804706.  
ACCESSION A79313  
VERSION A79313.1 GI:6092357  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Connor, S.E. and Whittle, N.R.  
TITLE POLYPEPTIDES USEFUL AS IMMUNOTHERAPEUTIC AGENTS AND METHODS OF  
JOURNAL POLYPEPTIDE PREPARATION  
Patent: WO 9804706-A 1 05-FEB-1998;  
FEATURES CANTAB PHARMA RES (GB)  
source location/Qualifiers  
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/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 6 a 8 c 13 g 7 t  
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Best Local Similarity 83.3%; Pred. No. 8.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 tcttcagtgccacagttgg 19  
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Db 13 TCTTCGTCGCCAGATGG 30

RESULT 11  
AR074516 34 bp DNA PAT 28-AUG-2000  
LOCUS AR074516 Sequence 1 from patent US 5955087;  
DEFINITION AR074516  
ACCESSION AR074516  
VERSION AR074516.1 GI:10001271  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Whittle, N. Richard, Carmichael, J. Paddon, Connor, S. Edward,  
Thompson, H. Stephengrammer and Wilson, M. Jonathan.  
TITLE Polypeptides useful as immunotherapeutic agents and methods of  
JOURNAL Polypeptide preparation  
Patent: US 5955087-A 1 21-SEP-1999;  
FEATURES location/Qualifiers  
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source /organism="unknown"

BASE COUNT 6 a 8 c 13 g 7 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 34;  
Best Local Similarity 83.3%; Pred. No. 8.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 tcttcagtgccacagttgg 19  
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Db 13 TCTTCGTCGCCAGATGG 30

RESULT 12  
I72347 16 bp DNA PAT 03-APR-1998  
LOCUS I72347 Sequence 3 from patent US 5683902.  
DEFINITION I72347  
ACCESSION I72347  
VERSION I72347.1 GI:3008486  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Hampel, A., DiPaolo, J., Siwkowski, A.M. and Galasinski, S.C.  
TITLE Human papilloma virus inhibition by a hairpin ribozyme  
JOURNAL Patent: US 5683902-A 3 04-NOV-1997;  
FEATURES location/Qualifiers  
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BASE COUNT 5 a 3 c 4 g 4 t

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 1.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ttcttcagtgccacagt 16  
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Db 16 TTCTTCAGGACACAGT 1

RESULT 13  
I72348 17 bp DNA PAT 03-APR-1998  
LOCUS I72348 Sequence 4 from patent US 5683902.  
DEFINITION I72348  
ACCESSION I72348  
VERSION I72348.1 GI:3008487  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Hampel, A., DiPaolo, J., Siwkowski, A.M. and Galasinski, S.C.  
TITLE Human papilloma virus inhibition by a hairpin ribozyme  
JOURNAL Patent: US 5683902-A 4 04-NOV-1997;  
FEATURES location/Qualifiers  
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source /organism="unknown"

BASE COUNT 6 a 3 c 4 g 4 t  
ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 17;  
Best Local Similarity 87.5%; Pred. No. 1.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ttcttcagtgccacagt 16  
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Db 16 TTCTTCAGGACACAGT 1

RESULT 14  
AX045082 20 bp DNA PAT 24-NOV-2000  
LOCUS AX045082 Sequence 12 from Patent WO0066149.  
DEFINITION AX045082  
ACCESSION AX045082  
VERSION AX045082.1 GI:11343681  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Gerhardt, C., Romero-Romero, I.A. and Strosberg, A.D.  
TITLE Medicines useful for treating disorders of regulation of body  
fatness and diseases related to disorders of leptin production  
JOURNAL Patent: WO 0066149-A 12 09-NOV-2000;  
FEATURES CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (FR)  
location/Qualifiers  
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/db\_xref="taxon:32630"  
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DB 16 TTCTTCAGCGCACACT 1

RESULT 15  
AX148237/C

LOCUS

AX148237 27 bp DNA

PAT

08-JUN-2001

DEFINITION

Sequence 78 from Patent WO0136471.

ACCESSION

AX148237

VERSION

AX148237.1 GI:14347135

KEYWORDS

SOURCE

synthetic construct.

ORGANISM

synthetic construct

REFERENCE

1 (bases 1 to 27)

AUTHORS

Chen, R., Dang, H.T. and Lowitz, K.P.

TITLE

Endogenous and non-endogenous versions of human g protein-coupled

JOURNAL

Patent: WO 0136471-A 78 25-MAY-2001;

FEATURES

Arena Pharmaceuticals, Inc. (US)

SOURCE

1. 27

BASE COUNT

/organism="synthetic construct"

ORIGIN

/db\_xref="taxon:32630"

BASE COUNT

/note="Novel Sequence"

ORIGIN

8 a 7 c 7 g 5 t

Query Match

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Best Local Similarity 87.5%; Pred. No. 1.5e+04;

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DB 20 TTCTTGAGTCCACACT 5

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Job time: 16637 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2001, 08:53:58 ; Search time 706.67 Seconds  
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Title: US-09-800-629A-52  
Perfect score: 20  
Sequence: 1 tttctcagtcgacagtttgt 20

Scoring table: IDENTITY\_NUC  
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Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 989696

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	20	100.0	20	21	AAC73699 Human IL-5 antisense
2	20	100.0	24	18	AAT75363 cDNA synthesis pri
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4	15.2	76.0	31	22	AAI30050 Human single nucle
5	14.4	72.0	24	14	AAQ53071 RBP receptor clone
6	13.8	69.0	25	12	AAQ10052 P4 primer specific
7	13.8	69.0	44	13	AAQ33937 Downstream sequenc
8	13.6	68.0	31	20	AAV33870 HPV-16 inhibitor.
9	13.6	68.0	31	20	AAV33873 HPV-16 inhibitor.
10	13.6	68.0	49	16	AAQ75472 HPV primer probe H
11	13.4	67.0	27	18	AAV68145 Human flt1 VEGF re

C	12	13.4	67.0	27	19	AAV95515 Human c-fos hamme
	13	13.4	67.0	43	21	AAA88735 Human FLINT mutage
	14	13.4	67.0	43	22	AAD07384 Mutagenic PCR prim
	15	13.4	67.0	47	21	AAZ67757 Human map-related
C	16	13.4	67.0	48	20	AAV22976 PCR primer tau-d1-
C	17	13.4	67.0	48	20	AAV70655 PCR primer tau-d1-
	18	13.2	66.0	30	18	AAT59419 Human papillomavir
C	19	13.2	66.0	31	19	AAV67604 Nucleotide fragmen
	20	13.2	66.0	31	19	AAV38943 Human genomic DNA
	21	13.2	66.0	34	17	AAV15139 Human papillomavir
	22	13.2	66.0	34	19	AAV39344 HPV-7 E7 gene PCR
C	23	13.2	66.0	50	16	AAQ75488 HPV primer probe H
	24	12.8	64.0	16	17	AAT40307 Human papilloma v1
	25	12.8	64.0	16	20	AAV33882 HPV-16 inhibitor.
	26	12.8	64.0	16	20	AAV33869 HPV-16 inhibitor.
	27	12.8	64.0	16	20	AAV33872 HPV-16 inhibitor.
C	28	12.8	64.0	16	20	AAV33867 HPV-16 inhibitor.
C	29	12.8	64.0	17	17	AAT40308 Human papilloma v1
	30	12.8	64.0	20	18	AAV12729 PCR primer cck77 for m
	31	12.8	64.0	20	18	AAT73498 PCR primer cck77 f
	32	12.8	64.0	20	19	AAV39225 PCR primer used to
	33	12.8	64.0	20	20	AAZ21983 Human alpha-chemok
C	34	12.8	64.0	20	22	AAAD12418 Human G-protein co
C	35	12.8	64.0	20	22	AAQ34345 AMG variant const
C	36	12.8	64.0	25	13	AAQ34345 Parasitic astacin
C	37	12.8	64.0	27	22	AAS07992 D. immitis nd1MPA2
	38	12.8	64.0	41	21	AAZ87894 RNA polymerase tra
	39	12.8	64.0	41	21	AAZ87894 Probe SNORF33h 90T
	40	12.6	63.0	29	17	AAT08971 S. venezuelae pik
C	41	12.6	63.0	29	17	AAT08971
	42	12.6	63.0	29	22	AAD11205
	43	12.6	63.0	31	16	AAQ90543
	44	12.6	63.0	31	18	AAT60010
	45	12.6	63.0	31	22	AAC90265
				32	21	AAZ87312

ALIGNMENTS

RESULT 1	
AACT73699	
ID AACT73699 standard; DNA; 20 BP.	
XX	
AC AACT73699;	
XX	
DT 02-FEB-2001 (first entry)	
XX	
DE Human IL-5 antisense oligonucleotide ISIS #16084.	
XX	
KW Human; interleukin-5; IL-5; signal transduction;	
KW antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;	
KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;	
KW inflammation; cancer; ss.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
PN WO200058512-A1.	
XX	
PD 05-OCT-2000.	
XX	
PF 17-MAR-2000; 2000WO-US07318.	
XX	
PR 26-MAR-1999; 99US-0280799.	
XX	
PA (ISIS-) ISIS PHARM INC.	
XX	
PI Dean NM, Karras JG, McKay R;	
XX	
DR WPI; 2000-594648/56.	
XX	
PT Antisense oligonucleotide compound used to treat asthma and	
PT eosinophilic syndrome in humans modulates interleukin-5 signal	

PT transduction -  
XX  
PS Claim 4; Page 63; 156pp; English.  
XX  
CC The present sequence is an oligonucleotide used for antisense  
CC modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides  
CC were designed to target nucleic acids encoding IL-5 and IL-5  
CC receptor-alpha. The antisense oligonucleotides may be used for the  
CC treatment of diseases associated with IL-5 signal transduction, IL-5  
CC expression or IL-5 receptor-alpha expression. Such diseases include  
CC asthma and eosinophilic syndrome. The oligonucleotides are also useful  
CC for research uses and to prevent or delay infection, inflammation or  
CC tumour formation.  
XX  
SQ Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 other;  
  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 ttcttcagtcacagttgt 20  
Db 1 ttcttcagtcacagttgt 20  
|||||  
  
RESULT 2  
AAT75363/c  
ID AAT75363 standard; CDNA; 24 BP.  
XX  
AC AAT75363  
XX  
DT 24-DEC-1998 (first entry)  
XX  
DE cDNA synthesis primer IL5-1.  
XX  
XX ss; human; RAD50; DNA repair; tumour suppression; cancer; Septin-2;  
KW central nervous system; PCR; primer; amplification.  
XX  
OS Synthetic.  
XX  
PN WO9727284-A2.  
XX  
PD 31-JUL-1997.  
XX  
PF 24-JAN-1997; 97WO-US01299.  
XX  
PR 17-JUL-1996; 96US-0687080.  
PR 26-JAN-1996; 96US-0592126.  
XX  
PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX  
PI Dolganov G;  
XX  
DR WPI; 1997-393672/36.  
XX  
PT Human tumour suppressor gene RAD50 - useful to detect  
PT predisposition to, decrease risk of and treat cancer, also Septin-2  
PT homologues  
XX  
PS Example 1; Page 36; 195pp; English.  
XX  
CC The primers AAT75354-T75378 were used to for cDNA synthesis in the  
CC method of the invention. Disclosed in the invention is human RAD50  
CC (hRAD50) which is involved in DNA repair and has tumour suppression  
CC activity, and can be used to detect predisposition to, decrease the risk  
CC of or treat cancers, e.g. acute myeloid leukaemia, myelodysplastic  
CC syndrome, therapy related myelodysplastic syndrome, therapy related  
CC acute myeloid leukaemia, refractory anaemia or refractory anaemia with  
CC excess blasts. Also disclosed in this invention are human Septin-2  
CC homologues which may be used as targets for cancer therapies and central  
CC nervous system directed treatment methods, and to measure the  
CC proliferative potential of selected cell types.

102

XX  
SQ Sequence 24 BP; 9 A; 7 C; 4 G; 4 T; 0 other;  
  
Query Match 100.0%; Score 20; DB 18; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 ttcttcagtcacagttgt 20  
Db 21 TTCTTCAGTCACAGTTGCT 2  
|||||  
  
RESULT 3  
AAV59945/c  
ID AAV59945 standard; DNA; 24 BP.  
XX  
AC AAV59945;  
XX  
DT 25-NOV-1998 (first entry)  
XX  
DE PCR primer IL5-1 used to amplify interleukin CDNA.  
XX  
KW Human analogue; yeast RAD50; Drosophila Septin-2; Acyl-CoA synthetase;  
KW immunomodulatory activity; identification; activated T-cell; cytokine;  
KW interleukin; IL; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9838306-A1.  
XX  
PD 03-SEP-1998.  
XX  
PF 27-FEB-1997; 97WO-US03159.  
XX  
PR 27-FEB-1997; 97WO-US03159.  
XX  
PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX  
PI Dolganov G;  
XX  
DR WPI; 1998-481207/41.  
XX  
PT Novel human immunomodulatory poly:peptide(s) - have homology to the  
PT yeast RAD50 or Drosophila Septin-2 proteins  
XX  
PS Example 1; Page 27; 155pp; English.  
XX  
CC PCR primers AAV59945-46 were used to identify cDNA encoding human  
CC cytokine interleukin (IL) from different cDNA pools, to provide an  
CC estimate of the degree to which the cytokine transcript is present. mRNA  
CC was isolated from activated T-cells, and converted to cDNA prior to  
CC amplification. The specification describes sequences encoding human  
CC analogues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA  
CC synthetase. The proteins have immunomodulatory activity. The nucleic  
CC acids and proteins can be used to identify activated T-cells in a sample  
CC population. They can also be used to isolate and identify sequences  
CC encoding other proteins or other compounds having immunomodulatory  
CC activity.  
XX  
SQ Sequence 24 BP; 9 A; 7 C; 4 G; 4 T; 0 other;  
  
Query Match 100.0%; Score 20; DB 19; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 ttcttcagtcacagttgt 20  
Db 21 TTCTTCAGTCACAGTTGCT 2  
|||||

17



```
RESULT 4
AAI30050/c
ID AAI30050 standard; DNA; 31 BP.
XX
XX AAI30050;
AC
XX 18-OCT-2001 (first entry)
DT
XX Human single nucleotide polymorphism (SNP) HRG 4.
DE
XX Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Variation replace(16,A)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200166800-A2.
PN
XX 13-SEP-2001.
PD
XX 07-MAR-2001; 2001WO-US07268.
PF
XX
XX 07-MAR-2000; 2000US-0187510.
PR
XX 22-MAY-2000; 2000US-0206129.
PA
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
PI
XX WPI; 2001-522952/57.
DR
XX
XX Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype
XX
XX Claim 1; Page 65; 145pp; English.
PS
XX
XX The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
XX Sequence 31 BP; 8 A; 12 C; 8 G; 3 T; 0 other;
SQ
Query Match 76.0%; Score 15.2; DB 22; Length 31;
Best Local Similarity 85.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 ttcttcagtcacagttggt 20
Db 28 TTCTTAAGTGCCACAGTGCT 9
RESULT 5
AAQ53071/c
ID AAQ53071 standard; cDNA to mRNA; 24 BP.
XX
XX AAQ53071;
AC
XX 30-AUG-1994 (first entry)
DT
XX RBP receptor clone extension.
DE
```

```
XX
XX Retinol binding protein; RBP; receptor; retinoid; retinitis;
KW clone; extension; ss.
XX
XX WO9323538-A.
PN
XX 25-NOV-1993.
PD
XX
XX 14-MAY-1993; 93WO-US04586.
PF
XX 15-MAY-1992; 92US-0883539.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Bavik CO, Eriksson U, Simon A, Bavik C;
PI
XX WPI; 1993-386570/48.
DR
XX
XX New retinol binding protein receptor and homologue coding nucleic
PT acid molecule - useful for diagnosis and treatment of retinoid
PT linked pathological conditions, for hybridisation in stringent
PT conditions and treating retinitis
XX
XX Claim 8; Page 15; 44pp; English.
PS
XX
XX Four extended clones of RBP receptor coding cDNA were isolated.
CC The extensions are given in AAQ53071-73 or is the sequence GAGAAA.
XX
XX Sequence 24 BP; 9 A; 5 C; 7 G; 3 T; 0 other;
SQ
Query Match 72.0%; Score 14.4; DB 14; Length 24;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 tcagtcacagttggt 20
Db 18 TCAGTCACACAGTGCT 3
RESULT 6
AAQ10052/c
ID AAQ10052 standard; DNA; 25 BP.
XX
XX AAQ10052;
AC
XX 14-MAR-1991 (first entry)
DT
XX P4 primer specific for HIV-2 ROD and SIVmac 142.
DE
XX HIV-2 ROD; SIV mac 142; genomic amplification; ss.
XX
XX WO9015158-A.
PN
XX
XX -13-DEC-1990.
PD
XX 05-JUN-1990; 90WO-FR00394.
PF
XX 02-JUN-1989; 89FR-0007355.
PR
XX (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST SANTE.
XX
XX Sonigo P, Brechot C, Courgnaud V;
PI
XX WPI; 1991-007227/01.
DR
XX
XX New oligo-nucleotide primers specific for HIV-2 or SIV mac -
PT useful in genomic amplification of viral nucleic acid before
PT detection by hybridisation test
XX
XX Claim 2; page 19; 32pp; French.
PS
XX
```

CC This primer (claimed) is specific for the fragment of HIV-2 ROD  
CC and SIV mac 142 cDNA covering bases 7782-7805 and 7776-7799 resp.  
CC It is used in a primer pair compsn., e.g. with primer LTR1, to  
CC amplify viral nucleic acid prior to detection using a hybridis-  
CC ation probe.  
CC See also AAQ10041-51 and AAQ10053-56.  
XX  
SQ Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 other;

Query Match 69.0%; Score 13.8; DB 12; Length 25;  
Best Local Similarity 88.2%; Pred. No. 5.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 ctctcagtcacagcttg 19  
||| ||||| |||  
Db 24 CTTTACGTGCACAGCTGC 8

RESULT 7

AAQ33937  
ID AAQ33937 standard; DNA; 44 BP.

AC AAQ33937;

DT 02-FEB-1993 (first entry)

DE Downstream sequence of microsatellite from clone TGLA34.

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.

OS Bos taurus.

PN WO9213102-A.

PD 06-AUG-1992.

PF 15-JAN-1992; 92WO-US00340.

PR 15-JAN-1991; 91US-0642342.

PA (GENM-) GENMARK.

PI Georges M, Massey JM;

DR WPI; 1992-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification,  
PT gene mapping, and selective breeding

PS Table 7; Page 304; 517pp; English.

CC The sequence is that downstream of a bovine microsatellite sequence  
CC obtd. by screening a library of bovine MboI DNA fragments of between  
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.  
CC One out of 50 clones cross-hybridised. Assuming independent  
CC distribution of microsatellites and MboI sites, the frequency of  
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,  
CC 000. The sequence information for ca. 230 such bovine microsatellites  
CC is summarised in the specification and indexed herein (see below).  
CC The sequences upstream and downstream of the microsatellite sequence  
CC were used to generate the required PCR primers for in vitro  
CC amplification of the corresp. microsatellite (using the program  
CC OPTIPRIM). The microsatellites may be used to identify individuals,  
CC for parentage testing, and in the genetic mapping of economic trait  
CC loci, or genes involved in the determination of economically important  
CC traits esp. in cattle, to allow selective breeding.  
CC See also AAQ33501-34437.

SQ Sequence 44 BP; 11 A; 13 C; 6 G; 14 T; 0 other;

Query Match 69.0%; Score 13.8; DB 13; Length 44;  
Best Local Similarity 88.2%; Pred. No. 5.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagct 17  
||||| ||||| |||  
Db 11 ttcttcagtcagct 27

RESULT 8

AAAX33870  
ID AAAX33870 standard; DNA; 31 BP.

AC AAAX33870;

DT 25-JUN-1999 (first entry)

DE HPV-16 inhibitor.

KW HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;  
KW keratinocyte; cervical cell; cervical tumour; ss.

OS Synthetic.

OS Human papillomavirus 16.

PN WO9913071-A1.

PD 18-MAR-1999.

PF 03-SEP-1998; 98WO-US18320.

PR 05-SEP-1997; 97US-0929140.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Alvarez-Salas L, DiPaolo J;

DR WPI; 1999-243727/20.

PT New antisense oligonucleotide analogs for inhibiting growth of  
PT cervical tumors

PS Claim 4; Page 36; 40pp; English.

CC This sequence represents an antisense oligonucleotide of the invention.  
CC The antisense oligonucleotide analogs (ONS) have a sequence complementary  
CC to a sequence of nucleotides 415-445 of human papilloma virus-16  
CC (HPV-16). The antisense ONS can be used to inhibit expression of HPV gene  
CC E6/E7 in living cells, preferably human keratinocytes or human cervical  
CC cells. They bind to E6/E7 mRNA in the cell, prevent mRNA translation  
CC and promote mRNA degradation by intracellular RNase H. They can be used  
CC for preventing transformation of living cells by HPV. The antisense ONS  
CC are used particularly for inhibiting the growth of cervical tumours.

SQ Sequence 31 BP; 8 A; 5 C; 7 G; 11 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 31;  
Best Local Similarity 80.0%; Pred. No. 6.9e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagctgt 20  
||||| ||||| |||  
Db 1 ttcttcagagacagctgt 20

RESULT 9

AAAX33873  
ID AAAX33873 standard; RNA; 31 BP.

AC AAAX33873;

DT 25-JUN-1999 (first entry)

XX DE HPV-16 Inhibitor.  
XX XX HPV-16; Inhibitor; antisense oligonucleotide; E6/E7 gene; human;  
KW keratinocyte; cervical cell; cervical tumour; ss.  
XX OS Synthetic.  
OS Human papillomavirus 16.  
XX PN WO913071-A1.  
XX PD 18-MAR-1999.  
XX PF 03-SEP-1998; 98WO-US18320.  
XX PR 05-SEP-1997; 97US-0929140.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Alvarez-Salas L, DiPaolo J;  
XX DR WPI; 1999-243727/20.  
XX PT New antisense oligonucleotide analogs for inhibiting growth of  
PT cervical tumors  
XX PS Claim 6; Page 35; 40pp; English.  
XX CC This sequence represents an antisense oligonucleotide of the invention.  
CC The antisense oligonucleotide analogs (ONS) have a sequence complementary  
CC to a sequence of nucleotides 415-445 of human papilloma virus-16  
CC (HPV-16). The antisense ONS can be used to inhibit expression of HPV gene  
CC E6/E7 in living cells, preferably human keratinocytes or human cervical  
CC cells. They bind to E6/E7 mRNA in the cell, prevent mRNA translation  
CC and promote mRNA degradation by intracellular RNase H. They can be used  
CC for preventing transformation of living cells by HPV. The antisense ONS  
CC are used particularly for inhibiting the growth of cervical tumours.  
XX SQ Sequence 31 BP; 8 A; 5 C; 7 G; 11 U; 0 other;  
  
Query Match 68.0%; Score 13.6; DB 20; Length 31;  
Best Local Similarity 50.0%; Pred. No. 6.9e+02;  
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
  
OY 1 ttcttcagtcacagtggt 20  
Db 1 uucucagagaacagugcu 20  
  
RESULT 10  
AAQ75472  
ID AAQ75472 standard; DNA; 49 BP.  
XX AC AAQ75472;  
XX DT 28-JUN-1995 (first entry)  
XX DE HPV primer probe HPV15.  
XX KW Human papilloma virus; HPV; HPV16; HPV18; diagnosis; primer; probe;  
KW hybridization; self-sustained sequence replication; 3SR;  
KW E6 protein; E7 protein; cervical dysplasia; cervix cancer; ss.  
XX OS Synthetic.  
XX PN WO9426934-A.  
XX PD 24-NOV-1994.  
XX PF 06-MAY-1994; 94WO-US05085.  
XX PR 06-MAY-1993; 93US-0058920.

XX PA (BAXT ) BAXTER DIAGNOSTICS INC.  
XX XX Brown JT;  
XX PI Brown JT;  
XX DR WPI; 1995-006821/01.  
XX PT Human papilloma virus detection assay - by amplification using  
PT self sustained sequence replication and hybridisation with a  
PT detector probe  
XX PS Disclosure; Page 10; 79pp; English.  
XX CC Self-sustained sequence replication is performed on HPV E6/E7  
CC region mRNA using 2 primers, one of which contains a  
CC transcriptional promoter, pref. the phage T7 RNA-polymerase  
CC binding site (AAQ75512). Suitable primers are given in AAQ75472-500.  
CC Amplified sequences are hybridized to capture probes (AAQ75501-05),  
CC and hybridization is detected using detection probes (AAQ75506-09,  
CC AAQ86975). Expression of E6/E7 is diagnostic for cervical cancer  
CC or pre-malignancy states.  
XX SQ Sequence 49 BP; 14 A; 10 C; 10 G; 15 T; 0 other;  
  
Query Match 68.0%; Score 13.6; DB 16; Length 49;  
Best Local Similarity 80.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
OY 1 ttcttcagtcacagtggt 20  
Db 30 ttcttcagacacagtggt 49  
  
RESULT 11  
AAQ68145/C  
ID AAX68145 standard; RNA; 27 BP.  
XX AC AAX68145;  
XX DT 28-JUL-1999 (first entry)  
XX DE Human flt1 VEGF receptor hammerhead ribozyme #871.  
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;  
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX OS Synthetic.  
OS Homo sapiens.  
XX PN WO9715662-A2.  
XX PD 01-MAY-1997.  
XX PF 25-OCT-1996; 96WO-US17480.  
XX PR 11-JAN-1996; 96US-0584040.  
XX PR 26-OCT-1995; 95US-0005974.  
XX PA (CHIR ) CHIRON CORP.  
PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;  
XX DR WPI; 1997-259017/23.  
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or  
PT mRNA stability - useful for treating e.g. tumour angiogenesis,  
PT psoriasis, rheumatoid arthritis, etc., in a human patient  
XX XX

PS Claim 9; Page 73; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can  
CC be treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention.  
XX  
SQ Sequence 27 BP; 11 A; 4 C; 6 G; 5 U; 1 other;  
  
Query Match 67.0%; Score 13.4; DB 18; Length 27;  
Best Local Similarity 93.3%; Pred. No. 8.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 tcttcagtcacagt 16  
DB 15 TCATCAGTCACACAGT 1  
  
RESULT 12  
AAV95515/c  
ID AAV95515 standard; RNA; 27 BP.  
XX  
AC AAV95515;  
XX  
DT 24-FEB-1999 (first entry)  
XX  
DE Human c-fos hammerhead ribozyme nucleotide position 1071.  
XX  
KW Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;  
KW cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;  
KW mutation; diseased cell; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9832846-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 20-JAN-1998; 98WO-US01017.  
XX  
PR 23-JAN-1997; 97US-0037658.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Jarvis T, McSwiggen JA, Stinchcomb DT;  
XX  
DR WPI; 1998-427942/36.  
XX  
PT Enzymatic nucleic acid molecules which specifically cleave RNA  
PT derived from a c-fos gene - useful for treating conditions related  
PT to levels of c-fos, especially cancer  
XX  
PS Claim 9; Page 51; 72pp; English.  
XX  
CC The present invention describes an enzymatic nucleic acid molecule which  
CC specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540  
CC and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin  
CC ribozymes, respectively, which specifically cleave human c-fos. AAV95261  
CC to AAV95400 and AAV95585 to AAV95628 represent human c-fos target  
CC sequences. The enzymatic nucleic acid molecules can be used for treating  
CC cancer associated with elevated levels of c-fos oncogene, especially  
CC leukaemias, neuroblastomas and lung, breast and colon cancers. The  
CC ribozymes may also be used as diagnostic tools to examine genetic drift  
CC and mutations within diseased cells, or to detect the presence of c-fos  
CC RNA in a cell.

XX  
SQ Sequence 27 BP; 7 A; 7 C; 7 G; 5 U; 1 other;  
  
Query Match 67.0%; Score 13.4; DB 19; Length 27;  
Best Local Similarity 93.3%; Pred. No. 8.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 tcttcagtcacagt 16  
DB 15 TCATCAGTCACACAGT 1  
  
RESULT 13  
AAA88735  
ID AAA88735 standard; DNA; 43 BP.  
XX  
AC AAA88735;  
XX  
DT 05-FEB-2001 (first entry)  
XX  
DE Human FLINT mutagenic primer CF 110.  
XX  
KW FLINT; FAS ligand inhibitory protein; human; protease resistant;  
KW acute lung injury; acute respiratory distress syndrome;  
KW chronic obstructive pulmonary disease; pulmonary fibrosis;  
KW ulcerative colitis; therapy; organ transplantation; mutagenesis;  
KW PCR primer; strand overlap extension; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200058466-A2.  
XX  
PD 05-OCT-2000.  
XX  
PF 20-MAR-2000; 2000WO-US06418.  
XX  
PR 30-MAR-1999; 99US-0126839.  
PR 21-JUN-1999; 99US-0140073.  
PR 04-AUG-1999; 99US-0147071.  
PR 20-OCT-1999; 99US-0160524.  
PR 21-OCT-1999; 99US-0160669.  
PR 20-DEC-1999; 99US-0172744.  
PR 26-JAN-2000; 2000US-0178184.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Micanovic R, Rathnachalam R, Witcher DR;  
XX  
DR WPI; 2000-664925/64.  
XX  
PT Novel protease resistant FAS ligand inhibitory protein analogues  
PT resistant to in vivo or in vitro proteolysis at amino acid position 218  
PT of the mature protein, useful for treating autoimmune diseases  
XX  
PS Example 1; Page 56; 100pp; English.  
XX  
CC The present sequence is that of primer D (CF 110) used with  
CC primers A (CF 107), B (CF 111) and C (CF 112) in a mutagenic PCR  
CC process, involving a strand overlap extension (SOE) reaction, to  
CC create a specific mutation in native FLINT cDNA (see AAA88730),  
CC producing an R218Q mutant in which Arg-218 of native FLINT (see  
CC AAB19705) is replaced by Gln (see AAB19709). The B and C primers are  
CC targeted to the same area of the FLINT gene but on opposite  
CC strands. Mismatch priming from both primers institutes the  
CC mutation. The products are used as template for the A to D  
CC reaction, which yields the desired mutated product. Claimed  
CC analogues of FLINT, including the R218Q mutant, are resistant  
CC to proteolytic cleavage, and are useful in the treatment of  
CC acute lung injury, acute respiratory stress syndrome, ulcerative  
CC colitis, chronic obstructive pulmonary disease, pulmonary  
CC fibrosis, to inhibit T lymphocyte activation, and to facilitate  
CC organ preservation for transplantation.

XX Sequence 43 BP; 13 A; 11 C; 14 G; 5 T; 0 other;  
SQ

Query Match 67.0%; Score 13.4; DB 21; Length 43;  
Best Local Similarity 93.3%; Pred. No. 9.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcttcagtgccacag 15  
||| |||||  
Db 9 ttcatcagtgccacag 23

RESULT 14  
AAD07384  
ID AAD07384 standard; DNA; 43 BP.  
XX  
AC AAD07384;  
XX  
DT 04-AUG-2001 (first entry)  
XX  
DE Mutagenic PCR primer D, CF110 to generate human FLINT variant, R218Q.  
XX  
KW Human: fas ligand inhibitory protein; FLINT; acute lung injury; ALI;  
KW TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;  
KW acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;  
KW chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;  
KW rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;  
KW fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;  
KW chronic renal failure; graft-vs-host disease; cutaneous inflammation;  
KW vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;  
KW insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;  
KW Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;  
KW Down's syndrome; multiple sclerosis; cytostatic; nootropic;  
KW neuroprotective; vasotropic; mutagenic PCR primer; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200142463-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 29-NOV-2000; 2000WO-US30166.  
XX  
PR 07-DEC-1999; 99US-0169367.  
PR 07-DEC-1999; 99US-0169381.  
PR 07-DEC-1999; 99US-0169412.  
PR 23-MAR-2000; 2000US-0191430.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Lu J, Witcher DR;  
XX  
DR WPI; 2001-381684/40.  
XX  
PT New FLINT polypeptide for treating and/or preventing acute lung injury,  
PT acute respiratory distress syndrome, ulcerative colitis, and  
PT graft-versus-host disease, comprises O-linked or N-linked  
PT oligosaccharides -  
XX  
PS Example 1; Page 32; 60pp; English.  
XX  
CC The present sequence is mutagenic reverse PCR primer D, CF110 which is  
CC used to generate human mature fas ligand inhibitory protein (FLINT)  
CC variant, R218Q. FLINT, a homologue of tumour necrosis factor receptor  
CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the  
CC interaction of FasL with fas. FLINT comprising O-linked or N-linked  
CC oligosaccharides is useful for preventing or treating acute lung injury  
CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,  
CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),  
CC to facilitate organ preservation for transplantation and to inhibit T  
CC lymphocyte activation. FLINT is useful for treating and/or preventing

CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,  
CC fibrotic lung disease, acute lung injury, human immunodeficiency virus  
CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-  
CC host disease, cutaneous inflammation, vascular leak syndrome,  
CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent  
CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,  
CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as  
CC psoriasis, Down's syndrome, and multiple sclerosis.  
XX  
SQ Sequence 43 BP; 13 A; 11 C; 14 G; 5 T; 0 other;  
XX

Query Match 67.0%; Score 13.4; DB 22; Length 43;  
Best Local Similarity 93.3%; Pred. No. 9.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcttcagtgccacag 15  
||| |||||  
Db 9 ttcatcagtgccacag 23

RESULT 15  
AAZ67757  
ID AAZ67757 standard; DNA; 47 BP.  
XX  
AC AAZ67757;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human map-related biallelic marker SEQ ID NO:2104.  
XX  
KW Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW diagnosis; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH key location/Qualifiers  
FH variation replace(24,T)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
PN WO9954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB00822.  
XX  
PR 21-APR-1998; 98US-0082614.  
PR 23-NOV-1998; 98US-0109732.  
XX  
PA (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
DR WPI; 2000-013267/01.  
XX  
PT Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome -  
XX  
PS Claim 1; Page 679; 2745pp; English.  
XX  
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the  
CC invention have a variety of uses: they can be used for high density  
CC mapping of the human genome, and in complex association studies and  
CC haplotyping studies which are useful in determining the genetic basis  
CC for disease states. Compositions and methods of the invention can also  
CC be useful for the identification of the targets for the development of  
CC pharmaceutical agents and diagnostic methods, as well as the

CC characterisation of the differential efficacious responses to and side  
CC effects from pharmaceutical agents acting on a disease as well as other  
CC treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297  
CC and 3367, are not actually given a sequence in the Sequence Listing  
CC from the present invention.

XX  
SQ Sequence 47 BP; 11 A; 11 C; 12 G; 13 T; 0 other;

Query Match 67.0%; Score 13.4; DB 21; Length 47;  
Best Local Similarity 93.3%; Pred. No. 9.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcttcagtgacacag 15  
|||||||  
DB 30 ttcttcagtgacacag 44

Search completed: December 26, 2001, 09:05:59  
Job time: 721 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:33:52 ; Search time 2376.51 Seconds  
(without alignments)  
138.835 Million cell updates/sec

Title: US-09-800-629A-62  
Perfect score: 20  
Sequence: 1 tctgcaaatgtcagatg 20

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 segs, 8248589755 residues

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_inv:\*  
32: em\_htgo\_rod:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	ARI36259	ARI36259 Sequence
2	20	100.0	33	6	I39778	I39778 Sequence
3	18.4	92.0	20	6	ARI36269	ARI36269 Sequence
4	15.2	76.0	20	6	ARI36270	ARI36270 Sequence
5	15	75.0	15	6	I39070	I39070 Sequence
6	14	70.0	15	6	I39071	I39071 Sequence
7	13.6	68.0	28	6	ARI06113	ARI06113 Sequence
8	12.8	64.0	50	6	AX157908	AX157908 Sequence
9	12.6	63.0	41	6	ARI11652	ARI11652 Sequence
10	12.6	63.0	41	6	ARI47013	ARI47013 Sequence
11	12.4	62.0	19	6	I17168	I17168 Sequence
12	12.4	62.0	21	4	DOG636A02	L27205 Dog primer
13	12.4	62.0	30	6	AR090348	AR090348 Sequence
14	12.4	62.0	33	6	AR086954	AR086954 Sequence
15	12.4	62.0	33	6	AR095649	AR095649 Sequence
16	12.4	62.0	33	6	ARI36117	ARI36117 Sequence
17	12.4	62.0	36	6	AR099138	AR099138 Sequence
18	12	60.0	20	6	ARI36271	ARI36271 Sequence
19	12	60.0	26	6	AX044220	AX044220 Sequence
20	12	60.0	26	6	AX044225	AX044225 Sequence
21	12	60.0	26	6	AX044241	AX044241 Sequence
22	12	60.0	26	6	AX044246	AX044246 Sequence
23	12	60.0	26	6	AX044283	AX044283 Sequence
24	12	60.0	26	6	AX044288	AX044288 Sequence
25	11.8	59.0	20	6	ARI36361	ARI36361 Sequence
26	11.8	59.0	21	6	AX096200	AX096200 Sequence
27	11.8	59.0	25	6	AX166679	AX166679 Sequence
28	11.8	59.0	26	6	AR089887	AR089887 Sequence
29	11.8	59.0	30	6	AX060834	AX060834 Sequence
30	11.8	59.0	48	6	AX191999	AX191999 Sequence
31	11.8	59.0	50	6	I15482	I15482 Sequence
32	11.6	58.0	21	6	I31287	I31287 Sequence
33	11.6	58.0	25	6	AR001070	AR001070 Sequence
34	11.6	58.0	25	6	AR075397	AR075397 Sequence
35	11.6	58.0	25	6	ARI42439	ARI42439 Sequence
36	11.6	58.0	31	6	AR063482	AR063482 Sequence
37	11.6	58.0	31	6	AR063484	AR063484 Sequence
38	11.6	58.0	43	9	HSU30443	U30443 Human tso1a
39	11.6	58.0	44	6	ARI01938	ARI01938 Sequence
40	11.6	58.0	45	3	BMOFIB5P	M10457 Bombyx mori
41	11.6	58.0	50	6	AX093077	AX093077 Sequence
42	11.4	57.0	39	6	A12211	A12211 EBI 660, 11
43	11.4	57.0	50	6	AX010685	AX010685 Sequence
44	11.2	56.0	20	6	A24703	A24703 Human tyros
45	11.2	56.0	20	6	ARI19566	ARI19566 Sequence

ALIGNMENTS

RESULT 1  
LOCUS ARI36259 20 bp DNA  
DEFINITION Sequence 62 from patent US 6136603.  
ACCESSION ARI36259  
VERSION ARI36259.1 GI:14476931  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean, N.M., Karras, J.G. and McKay, R.  
TITLE Antisense modulation of interleukin-5 signal transduction  
JOURNAL Patent: US 6136603-A 62 24-OCT-2000;  
FEATURES  
source location/Qualifiers  
1..20  
/organism="unknown"

Patent

BASE COUNT 5 a 3 c 6 g 6 t  
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtgatg 20  
|||||  
Db 1 TCTGGCAAAAGTGTCAGTATG 20

## RESULT 2

I39778/c

LOCUS I39778 33 bp DNA PAT 13-MAY-1997  
DEFINITION Sequence 51 from patent US 5616490.  
ACCESSION I39778  
VERSION I39778.1 GI:2084258

## KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 33)

TITLE Sullivan, S.M. and Draper, K.G.

JOURNAL Ribozymes targeted to TNF- $\alpha$ . RNAFEATURES Patent: US 5616490-A 51 01-APR-1997;  
Location/Qualifiers

source 1. .33

BASE COUNT 11 a 8 c 6 g 8 t

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtgatg 20  
|||||  
Db 28 TCTGGCAAAAGTGTCAGTATG 9

## RESULT 3

ARI36269

LOCUS ARI36269 20 bp DNA PAT 16-JUN-2001

DEFINITION Sequence 72 from patent US 6136603.

ACCESSION ARI36269

VERSION ARI36269.1 GI:14476941

## KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 20)

TITLE Dean, N.M., Karras, J.G. and McKay, R.

JOURNAL Antisense modulation of Interleukin-5 signal transduction

FEATURES Patent: US 6136603-A 72 24-OCT-2000;  
Location/Qualifiers

source 1. .20

BASE COUNT 5 a 4 c 5 g 6 t

## ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 20;  
Best Local Similarity 95.0%; Pred. No. 23;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtgatg 20  
|||||  
Db 1 TCTGGCAAAAGTGTCAGTATG 20

## RESULT 4

ARI36270

LOCUS ARI36270 20 bp DNA PAT 16-JUN-2001

DEFINITION Sequence 73 from patent US 6136603.  
ACCESSION ARI36270  
VERSION ARI36270.1 GI:14476942  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 20)

TITLE Dean, N.M., Karras, J.G. and McKay, R.

JOURNAL Antisense modulation of Interleukin-5 signal transduction

FEATURES Patent: US 6136603-A 73 24-OCT-2000;  
Location/Qualifiers

source 1. .20

BASE COUNT 4 a 5 c 4 g 7 t

## ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtgatg 20  
|||||  
Db 1 TCTGGCAACTCTCAGTATG 20

## RESULT 5

I39070/c

LOCUS I39070 15 bp DNA PAT 13-MAY-1997  
DEFINITION Sequence 108 from patent US 5616488.  
ACCESSION I39070  
VERSION I39070.1 GI:2083550

## KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 15)

TITLE Sullivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T.

JOURNAL IL-5 targeted ribozymes

FEATURES Patent: US 5616488-A 108 01-APR-1997;  
Location/Qualifiers

source 1. .15

BASE COUNT 4 a 4 c 3 g 4 t

## ORIGIN

Query Match 75.0%; Score 15; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtca 15  
|||||  
Db 15 TCTGGCAAAAGTGTCA 1

## RESULT 6

I39071/c

LOCUS I39071 15 bp DNA PAT 13-MAY-1997  
DEFINITION Sequence 109 from patent US 5616488.  
ACCESSION I39071  
VERSION I39071.1 GI:2083551

## KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 15)

TITLE Sullivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T.

JOURNAL IL-5 targeted ribozymes

FEATURES Patent: US 5616488-A 109 01-APR-1997;  
Location/Qualifiers

source 1. .15

BASE COUNT 5 a 4 c 3 g 3 t  
ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtc 14  
|||||  
Db 14 TCTGCCAAAGTGTC 1

RESULT 7  
ARI06113/c 28 bp DNA PAT 14-FEB-2001  
LOCUS ARI06113 Sequence 9 from patent US 6103514.  
ACCESSION ARI06113  
VERSION ARI06113.1 GI:12820178  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Natori, S.  
TITLE Protease  
JOURNAL Patent: US 6103514-A 9 15-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..28  
BASE COUNT 10 a 8 c 5 g 5 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 28;  
Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtatg 20  
|||||  
Db 23 TCTGCCACTGTGTCATATG 4

RESULT 8  
LOCUS AX157908 50 bp DNA PAT 22-JUN-2001  
DEFINITION Sequence 1236 from Patent WO0140521.  
ACCESSION AX157908  
VERSION AX157908.1 GI:14539239  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 1236 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..50  
misc\_feature /organism="Homo sapiens"  
25..26 /db\_xref="taxon:9606"  
misc\_feature /note="Nucleotide deleted between bases 25 and 26  
Accession number cg28396311"  
26

BASE COUNT 10 a 12 c 19 g 9 t  
ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 50;  
Best Local Similarity 87.5%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcag 16  
|||||  
Db 25 TCCCGCAAGTGTCAG 10

RESULT 9  
ARI11652 41 bp DNA PAT 14-FEB-2001  
LOCUS ARI11652 Sequence 186 from patent US 6127163.  
DEFINITION ARI11652  
ACCESSION ARI11652  
VERSION ARI11652.1 GI:12828500  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 41)  
AUTHORS Cochran, M.D. and Junker, D.E.  
TITLE Recombinant swinepox virus  
JOURNAL Patent: US 6127163-A 186 03-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..41  
BASE COUNT 17 a 5 c 6 g 13 t  
ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 41;  
Best Local Similarity 78.9%; Pred. No. 3.8e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtat 19  
|||||  
Db 8 TCTGCCATTGTGTATTAT 26

RESULT 10  
LOCUS ARI47013 41 bp DNA PAT 08-AUG-2001  
DEFINITION Sequence 74 from patent US 6221361.  
ACCESSION ARI47013  
VERSION ARI47013.1 GI:15110816  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 41)  
AUTHORS Cochran, M.D. and Junker, D.E.  
TITLE Recombinant swinepox virus  
JOURNAL Patent: US 6221361-A 74 24-APR-2001;  
FEATURES Location/Qualifiers  
source 1..41  
BASE COUNT 17 a 5 c 6 g 13 t  
ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 41;  
Best Local Similarity 78.9%; Pred. No. 3.8e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtat 19  
|||||  
Db 8 TCTGCCATTGTGTATTAT 26

RESULT 11  
LOCUS 117168/c 117168 19 bp DNA PAT 03-APR-1996

DEFINITION Sequence 23 from patent US 5484886.  
ACCESSION 117168  
VERSION 117168.1 GI:1252076  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 19)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 23 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..19  
BASE COUNT 5 a 7 c 1 g 6 t  
ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 aaagtgtcagtatg 20  
Db 18 AAAGGTCAGTATG 5

RESULT 12  
DOGP636A02  
LOCUS DOGP636A02 21 bp DNA MAM 19-JAN-1996  
DEFINITION Dog primer for STS 636, 3' end.  
ACCESSION L27205  
VERSION L27205.1 GI:439191  
KEYWORDS PCR Identification; PCR primer; STS.  
SEGMENT 2 of 2  
SOURCE Canis familiaris (library: E. Ostrander, in pbluescript+) adult spleen DNA.  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 21)  
Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.  
TITLE One hundred and one new simple sequence repeat-based markers for the canine genome  
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)  
MEDLINE 95268214  
COMMENT Submitted by:  
Fred Hutchinson Cancer Research Center  
Transplantation Biology Dept  
1124 Columbia; Mailstop M318  
Seattle, WA 98104, USA  
e-mail: eoststrand@fred.fhcrc.org  
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)  
PCR Profile: Denaturation: 94 degrees C for 1.00 minute  
Annealing: 55 or 59 degrees C for 0.45 minutes  
Polymerization: 74 degrees C for 1.00 minutes  
PCR Cycles: 33  
Final Extension: 74 degrees C for 5.00 minutes.  
FEATURES Location/Qualifiers  
source 1..21  
/organism="Canis familiaris"  
/db\_xref="taxon:9615"  
/dev\_stage="adult"  
/tissue\_type="spleen"  
/tissue\_lib="E. Ostrander, in pbluescript+"  
primer\_bind 8 a 4 c 5 g 4 t  
BASE COUNT 8 a 4 c 5 g 4 t  
ORIGIN

Query Match 62.0%; Score 12.4; DB 4; Length 21;  
Best Local Similarity 92.9%; Pred. No. 4.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctggcaaatgttca 15  
Db 1 CTGCCAAGTGTCA 14

RESULT 13  
AR090348  
LOCUS AR090348 30 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 468 from patent US 5994076.  
ACCESSION AR090348  
VERSION AR090348.1 GI:10017103  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 30)  
AUTHORS Chenchik,A., Jokhadze,G. and Biblilashvilli,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 468 30-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..30  
BASE COUNT 11 a 5 c 10 g 4 t  
ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 30;  
Best Local Similarity 92.9%; Pred. No. 4.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tggcaaatgttcag 16  
Db 15 TGGCAAGTGTGAG 28

RESULT 14  
AR086954  
LOCUS AR086954 33 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 4 from patent US 5985646.  
ACCESSION AR086954  
VERSION AR086954.1 GI:10013720  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 33)  
AUTHORS Murphy,D., Reid,J. and Robertson,D.  
TITLE Amidase  
JOURNAL Patent: US 5985646-A 4 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..33  
BASE COUNT 13 a 8 c 7 g 5 t  
ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 33;  
Best Local Similarity 92.9%; Pred. No. 4.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctggcaaatgttca 15  
Db 15 CTGGCAGTGTGCA 28

RESULT 15  
AR095649  
LOCUS AR095649 33 bp DNA PAT 08-SEP-2000  
DEFINITION Sequence 4 from patent US 6004796.  
ACCESSION AR095649  
VERSION AR095649.1 GI:10023712  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Murphy, D., Reid, J. and Robertson, D.  
TITLE Amidase  
JOURNAL Patent: US 6004796-A 4 21-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..33  
BASE COUNT 13 a 8 c 7 g 5 t  
ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 33;  
Best Local Similarity 92.9%; Pred. No. 4.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ctggcgaagtgtca 15  
||||| |||||  
Db 15 CTGGCAGCTGTCA 28

Search completed: December 21, 2001, 11:33:53  
Job time: 16640 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 08:38:29 ; Search time 303.16 Seconds  
(without alignments)  
14.941 Million cell updates/sec

Title: US-09-800-629A-52  
Perfect score: 20  
Sequence: 1 ttcttcagtcacagttgt 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	20	3	US-09-280-799-52 Sequence 52, Appl
2	20	100.0	24	1	US-08-592-126-14 Sequence 14, Appl
3	20	100.0	24	2	US-08-687-080-14 Sequence 14, Appl
4	14.4	72.0	24	1	US-08-200-807-3 Sequence 3, Appl
5	14.4	72.0	24	1	US-08-488-305A-3 Sequence 3, Appl
6	13.8	69.0	25	3	US-08-343-998-12 Sequence 12, Appl
7	13.6	68.0	31	3	US-08-929-140-16 Sequence 16, Appl
8	13.6	68.0	31	3	US-08-929-140-17 Sequence 17, Appl
9	13.6	68.0	31	4	US-09-560-579A-16 Sequence 16, Appl
10	13.6	68.0	31	4	US-09-560-579A-17 Sequence 17, Appl
11	13.6	68.0	49	5	PCT-US94-05085A-3 Sequence 3, Appl
12	13.6	68.0	49	5	PCT-US94-05085A-3 Sequence 3, Appl
13	13.4	67.0	27	3	US-08-998-099-255 Sequence 255, App
14	13.2	66.0	34	2	US-08-606-288-1 Sequence 1, Appl
15	13.2	66.0	34	3	US-09-347-483-1 Sequence 1, Appl
16	13.2	66.0	50	5	PCT-US94-05085A-19 Sequence 19, Appl
17	13.2	66.0	50	5	PCT-US94-05085A-19 Sequence 19, Appl
18	12.8	64.0	16	1	US-08-410-005-3 Sequence 3, Appl
19	12.8	64.0	16	3	US-08-929-140-3 Sequence 3, Appl
20	12.8	64.0	16	3	US-08-929-140-5 Sequence 5, Appl
21	12.8	64.0	16	3	US-08-929-140-7 Sequence 7, Appl
22	12.8	64.0	16	4	US-09-560-579A-3 Sequence 3, Appl
23	12.8	64.0	16	4	US-09-560-579A-5 Sequence 5, Appl
24	12.8	64.0	16	4	US-09-560-579A-7 Sequence 7, Appl
25	12.8	64.0	17	1	US-08-410-005-4 Sequence 4, Appl
26	12.8	64.0	20	4	US-09-042-353-341 Sequence 341, App
27	12.8	64.0	20	4	US-09-487-445-104 Sequence 104, App

28	12.8	64.0	20	4	US-08-758-417A-189 Sequence 189, App
29	12.8	64.0	50	5	PCT-US94-05085A-20 Sequence 20, Appl
30	12.8	64.0	50	5	PCT-US94-05085-20 Sequence 20, Appl
31	12.6	63.0	29	1	US-08-463-262A-17 Sequence 17, Appl
32	12.6	63.0	29	1	US-08-463-989-17 Sequence 17, Appl
33	12.6	63.0	29	4	US-09-003-574-17 Sequence 17, Appl
34	12.6	63.0	29	4	US-09-003-570-17 Sequence 31, Appl
35	12.6	63.0	29	4	US-08-584-760A-31 Sequence 31, Appl
36	12.6	63.0	31	1	US-08-524-757-34 Sequence 34, Appl
37	12.6	63.0	40	4	US-08-584-760A-32 Sequence 32, Appl
38	12.6	63.0	41	1	US-08-333-894-1 Sequence 1, Appl
39	12.4	62.0	25	4	US-08-638-931-22 Sequence 22, Appl
40	12.4	62.0	27	3	US-08-765-332-57 Sequence 57, Appl
41	12.2	61.0	20	4	US-09-487-445-30 Sequence 30, Appl
42	12.2	61.0	24	1	US-08-175-155-44 Sequence 44, Appl
43	12.2	61.0	24	1	US-08-477-509B-79 Sequence 79, Appl
44	12.2	61.0	24	2	US-08-707-237A-50 Sequence 50, Appl
45	12.2	61.0	24	3	US-08-482-085B-79 Sequence 79, Appl

## ALIGNMENTS

RESULT 1  
US-09-280-799-52  
Sequence 52, Application US/09280799  
Patent No. 6136603  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Karra, James G  
APPLICANT: McKay, Robert  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
FILE OF INVENTION: TRANSDUCTION  
FILE REFERENCE: ISPH-0340  
CURRENT APPLICATION NUMBER: US/09/280,799  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 52  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-280-799-52

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttcttcagtcacagttgt 20  
Db 1 ttcttcagtcacagttgt 20

RESULT 2  
US-08-592-126-14/c  
Sequence 14, Application US/08592126  
Patent No. 5821091  
GENERAL INFORMATION:  
APPLICANT: Gregory Dolganov  
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:



```

; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,126
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Primer IL5-1
;
US-08-592-126-14
;
Query Match      100.0%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttggt 20
   ||||||||||||||||
Db 21 TTCTTCAGTCACAGTTGCT 2

RESULT 3
US-08-687-080-14/c
; Sequence 14, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Primer IL5-1
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US-08-687-080-14
;
Query Match      100.0%; Score 20; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttggt 20
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Db 21 TTCTTCAGTCACAGTTGCT 2

RESULT 4
US-08-200-807-3/c
; Sequence 3, Application US/08200807
; Patent No. 5573939
; GENERAL INFORMATION:
; APPLICANT: B vik, Claes Olof, Eriksson, Ulf
; TITLE OF INVENTION: Isolated Protein Receptors, Antibodies which
; TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
; Patent No. 5573939
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,807
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/883,539
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5573939man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
;
US-08-200-807-3
;
Query Match      72.0%; Score 14.4; DB 1; Length 24;
Best Local Similarity 93.8%; Pred. No. 77;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 tcagtcacagttgt 20  
|||||  
Db 18 TCAGTCCACAGTTGGT 3

## RESULT 5

US-08-488-305A-3/C

; Sequence 3, Application US/08488305A

; Patent No. 5679772

; GENERAL INFORMATION:

; APPLICANT: B vik, Claes Olof; Eriksson, Ulf; Peterson, Per A.

; TITLE OF INVENTION: Isolated Protein Receptors, Antibodies which

; TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding

; Patent No. 5679772

; TITLE OF INVENTION: Therefor, And Uses Thereof

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte &amp; Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,305A

; FILING DATE: 7-JUNE-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kohl, Vineet

; REGISTRATION NUMBER: 37,003

; REFERENCE/DOCKET NUMBER: LUD 5280.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA to mRNA

; HYPOTHETICAL: no

; ANTI-SENSE: no

US-08-488-305A-3

Query Match 72.0%; Score 14.4; DB 1; Length 24;

Best Local Similarity 93.8%; Pred. No. 77;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 tcagtcacagttgt 20  
|||||

Db 18 TCAGTCCACAGTTGGT 3

## RESULT 6

US-08-343-998-12/C

; Sequence 12, Application US/08343998A

; Patent No. 6020123

; GENERAL INFORMATION:

; APPLICANT: Sonigo, Pierre

; APPLICANT: Brechot, Christian

; APPLICANT: Courgnard, Valerie

; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES FOR THE AMPLIFICATION OF THE

; TITLE OF INVENTION: GENOME OF THE RETROVIRUSES OF THE HIV-2 AND SIV TYPE,

; TITLE OF INVENTION: AND THEIR USES FOR IN VITRO DIAGNOSIS OF THE INFECTIONS

; TITLE OF INVENTION: DUE TO THESE VIRUSES

; FILE REFERENCE: 2356.0065-01

; CURRENT APPLICATION NUMBER: US/08/343,998A

; CURRENT FILING DATE: 1994-11-18

; EARLIER APPLICATION NUMBER: 07/820,600

; EARLIER FILING DATE: 1992-01-22

; EARLIER APPLICATION NUMBER: PCT/FR90/00394

; EARLIER FILING DATE: 1990-06-05

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO: 12

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 2

; FEATURE:

US-08-343-998-12

Query Match 69.0%; Score 13.8; DB 3; Length 25;

Best Local Similarity 88.2%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 cttagtcacagttgg 19  
|||

Db 24 CTTAGTCCACAGTGG 8

## RESULT 7

US-08-929-140-16

; Sequence 16, Application US/08929140

; Patent No. 6084090

; GENERAL INFORMATION:

; APPLICANT: DiPaolo, Joseph

; APPLICANT: Alvarez-Salas, Luis

; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson &amp; Bear

; STREET: 620 Newport Center Drive Sixteenth Flo

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/929,140

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER: NIH138.001A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 714/760-0404

; TELEFAX: 714/760-9503

; TELEX:

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 31 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

US-08-929-140-16



APPLICATION NUMBER: US/09/560,579A  
FILING DATE: 28-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/929,140  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: NIH138.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714/760-0404  
TELEFAX: 714/760-9503  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-560-579A-17

Query Match 68.0%; Score 13.6; DB 4; Length 31;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttggt 20  
||||||| | ||||| | |  
Db 1 TTCTTCAGACAGACAGTGCGT 20

RESULT 11  
PCT-US94-05085A-3  
Sequence 3, Application PC/TUS9405085A  
GENERAL INFORMATION:  
APPLICANT: Janice T. Brown  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS DETECTION ASSAY  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Baxter Diagnostics Inc.  
STREET: One Baxter Parkway, Building DP-3E  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.0  
SOFTWARE: Macintosh Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05085A  
FILING DATE: N/A  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/058,920  
FILING DATE: May 6, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Buonaiuto  
REGISTRATION NUMBER: 31,593  
REFERENCE/DOCKET NUMBER: BA-4448  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708/948-2537  
TELEFAX: 708/948-2642  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE:  
DESCRIPTION: Other nucleic acid, synthetic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
IMMEDIATE SOURCE:  
LIBRARY: DNA synthesizer  
FEATURE:  
NAME/KEY: HPV15. Phage T7 RNA polymerase binding site at 5'end, followed by  
PCT-US94-05085A-3

Query Match 68.0%; Score 13.6; DB 5; Length 49;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagttggt 20  
||||||| | ||||| | |  
Db 30 TTCTTCAGACAGACAGTGCGT 49

RESULT 12  
PCT-US94-05085-3  
Sequence 3, Application PC/TUS9405085  
GENERAL INFORMATION:  
APPLICANT: Janice T. Brown  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS DETECTION ASSAY  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Baxter Diagnostics Inc.  
STREET: One Baxter Parkway, Building DP-3E  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.0  
SOFTWARE: Macintosh Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05085  
FILING DATE: 06-MAY-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/058,920  
FILING DATE: May 6, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Buonaiuto  
REGISTRATION NUMBER: 31,593  
REFERENCE/DOCKET NUMBER: BA-4448  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708/948-2537  
TELEFAX: 708/948-2642  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: Other nucleic acid, synthetic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
IMMEDIATE SOURCE:  
LIBRARY: DNA synthesizer  
FEATURE:  
NAME/KEY: HPV15. Phage T7 RNA polymerase binding site at 5'end, followed by  
PCT-US94-05085-3

Query Match 68.0%; Score 13.6; DB 5; Length 49;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



ATTORNEY/AGENT INFORMATION:  
NAME: Walter H. Dreger  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63284/MHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-347-483-1

Query Match 66.0%; Score 13.2; DB 3; Length 34;  
Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 tcttcagtgacacaglttg 19  
||||| ||||| ||| |||  
DB 13 TCTTCGCGTGGCGCAGATGG 30

Search completed: December 21, 2001, 11:39:04  
Job time: 10835 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:39:05 ; Search time 303.16 Seconds  
(without alignments)  
14.941 Million cell updates/sec

Title: US-09-800-629A-62  
Perfect score: 20  
Sequence: 1 tctgcaaaagtgtcagatg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-280-799-62
2	20	100.0	33	1	US-08-434-503-51
3	18.4	92.0	20	3	US-09-280-799-72
4	15.2	76.0	20	3	US-09-280-799-73
5	15	75.0	15	1	US-08-319-492B-108
6	14	70.0	15	1	US-08-319-492B-109
7	13.6	68.0	28	3	US-09-120-365-9
8	13.6	68.0	28	4	US-09-515-039-9
9	12.6	63.0	41	3	US-08-480-640A-186
10	12.6	63.0	41	3	US-08-295-802-186
11	12.6	63.0	41	4	US-08-686-968C-74
12	12.6	63.0	41	4	US-08-488-237A-186
13	12.4	62.0	19	1	US-08-117-965-23
14	12.4	62.0	30	2	US-08-859-998-468
15	12.4	62.0	33	2	US-08-664-646A-4
16	12.4	62.0	33	2	US-09-066-285-4
17	12.4	62.0	33	3	US-09-261-006-4
18	12.4	62.0	33	3	US-08-951-088-4
19	12.4	62.0	36	3	US-09-023-082A-3
20	12.2	61.0	18	3	US-09-344-520-39
21	12.2	61.0	21	6	5455029-28
22	12	60.0	20	3	US-09-280-799-74
23	12	60.0	35	4	US-09-428-292-9
24	11.8	59.0	20	3	US-09-280-799-164
25	11.8	59.0	26	2	US-08-859-998-7
26	11.8	59.0	50	1	US-08-178-606-11
27	11.6	58.0	21	1	US-08-222-177A-199

c	28	11.6	58.0	21	4	US-09-019-160-79	Sequence 79, Appl
c	29	11.6	58.0	25	1	US-08-438-753B-14	Sequence 14, Appl
c	30	11.6	58.0	25	1	US-08-443-883A-14	Sequence 14, Appl
c	31	11.6	58.0	25	2	US-08-631-328-14	Sequence 14, Appl
c	32	11.6	58.0	25	2	US-08-455-524B-14	Sequence 14, Appl
c	33	11.6	58.0	25	2	US-08-455-021B-14	Sequence 14, Appl
c	34	11.6	58.0	25	4	US-09-045-467-14	Sequence 14, Appl
c	35	11.6	58.0	31	2	US-08-077-251-6	Sequence 6, Appl1
c	36	11.6	58.0	31	2	US-08-077-251-6	Sequence 6, Appl1
c	37	11.6	58.0	44	3	US-08-989-251-11	Sequence 11, Appl
c	38	11.6	58.0	44	3	US-09-340-250-11	Sequence 94, Appl
c	39	11.4	57.0	18	4	US-08-478-316-94	Sequence 537, App
c	40	11.4	57.0	19	4	US-09-338-907-537	Sequence 26, Appl
c	41	11.4	57.0	24	2	US-08-360-606B-26	Sequence 24, Appl
c	42	11.4	57.0	30	4	US-09-230-199-24	Sequence 220, App
c	43	11.4	57.0	47	4	US-09-338-907-220	Sequence 297, App
c	44	11.4	57.0	47	4	US-09-338-907-297	Sequence 7, Appl1
c	45	11.2	56.0	20	3	US-08-987-326-7	

ALIGNMENTS

RESULT 1  
US-09-280-799-62  
; Sequence 62, Application US/09280799  
; Patent No. 6136603  
GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Karris, James G.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION  
; FILE REFERENCE: ISPH-0340  
; CURRENT APPLICATION NUMBER: US/09/280,799  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-280-799-62

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred No. 0.029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgcaaaagtgtcagatg 20  
Db 1 tctgcaaaagtgtcagatg 20

RESULT 2  
US-08-434-503-51/c  
; Sequence 51, Application US/08434503  
; Patent No. 5616490  
GENERAL INFORMATION:  
; APPLICANT: Sean M. Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: TREATMENT OF INFLAMMATORY  
; TITLE OF INVENTION: DISEASE  
; NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA

Art

ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,503  
FILING DATE: 04-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,895  
FILING DATE: 19-JAN-1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 200/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-434-503-51

Query Match 100.0%; Score 20; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtatg 20  
|||||  
DB 28 TCTGGCAAAGTGTCAGTATG 9

RESULT 3  
US-09-280-799-72  
Sequence 72, Application US/09280799  
Patent No. 6136603  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Kairas, James G  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
TITLE OF INVENTION: TRANSDUCTION  
FILE REFERENCE: ISPH-0340  
CURRENT APPLICATION NUMBER: US/09/280,799  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 72  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-280-799-72

Query Match 92.0%; Score 18.4; DB 3; Length 20;  
Best Local Similarity 95.0%; Pred. No. 0.21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtatg 20  
|||||  
DB 1 tctggcaaatgtcagtatg 20

RESULT 4  
US-09-280-799-73  
Sequence 73, Application US/09280799  
Patent No. 6136603  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Kairas, James G  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
TITLE OF INVENTION: TRANSDUCTION  
FILE REFERENCE: ISPH-0340  
CURRENT APPLICATION NUMBER: US/09/280,799  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 73  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-280-799-73

Query Match 76.0%; Score 15.2; DB 3; Length 20;  
Best Local Similarity 85.0%; Pred. No. 11;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagtatg 20  
|||||  
DB 1 tctggcatactctcagtatg 20

RESULT 5  
US-08-319-492B-108/c  
Sequence 108, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard

Two

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-319-492B-108

Query Match 75.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaaagtgtca 15  
|||||  
Db 15 TCTGCCAAGTGTCA 1

RESULT 6  
US-08-319-492B-109/c  
Sequence 109, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-319-492B-109

Query Match 70.0%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaaagtgtc 14  
|||||  
Db 14 TCTGCCAAGTGTCT 1

RESULT 7  
US-09-120-365-9/c  
Sequence 9, Application US/09120365  
Patent No. 6103514  
GENERAL INFORMATION:  
APPLICANT: Natori, Shunji  
TITLE OF INVENTION: NEW PROTEASE  
FILE REFERENCE: 32290-144749  
CURRENT APPLICATION NUMBER: US/09/120,365  
EARLIER FILING DATE: 1998-07-22  
EARLIER APPLICATION NUMBER: JP 9-333 474  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 9  
LENGTH: 28  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-120-365-9

Query Match 68.0%; Score 13.6; DB 3; Length 28;  
Best Local Similarity 80.0%; Pred. No. 85;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctggcaaaagtgtcagtgtg 20  
|||||  
Db 23 TCTGCCACTGTGTCCATATG 4

RESULT 8  
US-09-515-039-9/c  
Sequence 9, Application US/09515039  
Patent No. 6214599  
GENERAL INFORMATION:  
APPLICANT: Natori, Shunji  
TITLE OF INVENTION: NEW PROTEASE  
FILE REFERENCE: 32290-144749  
CURRENT APPLICATION NUMBER: US/09/515,039  
EARLIER FILING DATE: 2000-03-06  
EARLIER APPLICATION NUMBER: JP 9-333 474  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 9  
LENGTH: 28  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-515-039-9

Query Match 68.0%; Score 13.6; DB 4; Length 28;  
Best Local Similarity 80.0%; Pred. No. 85;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctgccaagtgtcagtatg 20  
||||| ||||| |||||  
Db 23 TCTGCCACTGTGTCCATATG 4

## RESULT 9

US-08-480-640A-186

Sequence 186, Application US/08480640A

Patent No. 6033904

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

APPLICANT: Junker, David E.

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,640A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-480-640A-186

Query Match 63.0%; Score 12.6; DB 3; Length 41;

Best Local Similarity 78.9%; Pred. No. 3.2e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctgccaagtgtcagtat 19  
||||| ||||| |||||

Db 8 TCTGCCACTGTGTATTAT 26

## RESULT 10

US-08-295-802-186

Sequence 186, Application US/08295802

Patent No. 6127163

GENERAL INFORMATION:

APPLICANT: Cochran Ph.D., Mark D

APPLICANT: Junker M.S., David E

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 188

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/295,802

FILING DATE: Herewith

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)977-9550

TELEFAX: (212)664-0525

TELEX: 422523

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-295-802-186

Query Match 63.0%; Score 12.6; DB 3; Length 41;

Best Local Similarity 78.9%; Pred. No. 3.2e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctgccaagtgtcagtat 19  
||||| -||||| |||||

Db 8 TCTGCCACTGTGTATTAT 26

## RESULT 11

US-08-686-968C-74

Sequence 74, Application US/08686968C

Patent No. 6221361

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

APPLICANT: Junker, David E.

TITLE OF INVENTION: Recombinant Swinepox Virus

FILE REFERENCE: 39119-H/JML

CURRENT APPLICATION NUMBER: US/08/686,968C

CURRENT FILING DATE: 1996-07-25

NUMBER OF SEQ ID NOS: 231

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 74

LENGTH: 41

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-686-968C-74

Query Match 63.0%; Score 12.6; DB 4; Length 41;

Best Local Similarity 78.9%; Pred. No. 3.2e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctgccaagtgtcagtat 19  
||||| ||||| |||||

Db 8 tctgcatgtgtattat 26

## RESULT 12

US-08-488-237A-186

Sequence 186, Application US/08488237A

Patent No. 6251403

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,237A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 186:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-488-237A-186

Query Match 63.0%; Score 12.6; DB 4; Length 41;  
Best Local Similarity 78.9%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctggcaaaagtgtagtat 19  
||||||| ||||| ||||  
Db 8 TCTGCAATTGTGTATTAT 26

RESULT 13  
US-08-117-965-23/c  
Sequence 23, Application US/08117965  
Patent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
APPLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197

FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-23

Query Match 62.0%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 aaagtgcagtatg 20  
||||| ||||| |||||  
Db 18 AAAGGTCAGTATG 5

RESULT 14  
US-08-859-998-468  
Sequence 468, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Johhadze, George  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 468:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer

US-08-859-998-468

Query Match 62.0%; Score 12.4; DB 2; Length 30;  
Best Local Similarity 92.9%; Pred. No. 3.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 tggcacaagtgtcag 16  
|||||  
Db 15 TGGCAAGTGTGAG 28

## RESULT 15

US-08-664-646A-4  
; Sequence 4, Application US/08664646A  
; Patent No. 5877001  
; GENERAL INFORMATION:  
; APPLICANT: Murphy et al.  
; TITLE OF INVENTION: Amidases  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/664,646A  
; FILING DATE: June 17, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Charles J. Herron  
; REGISTRATION NUMBER: 28,019  
; REFERENCE/DOCKET NUMBER: 331400-53  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 NUCLEOTIDES  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: Oligonucleotide  
; US-08-664-646A-4

Query Match 62.0%; Score 12.4; DB 2; Length 33;  
Best Local Similarity 92.9%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctggcaaatgttca 15  
|||||  
Db 15 CTGCACAGTGTCA 28

Search completed: December 21, 2001, 11:39:06  
Job time: 10837 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:34:01 ; Search time 2376.51 Seconds

(without alignments)  
104.127 Million cell updates/sec

Title: US-09-800-629A-209

Perfect score: 15

Sequence: 1 tctaccaagacttc 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues 541028

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_inv:\*  
32: em\_htgo\_rod:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	15	100.0	20	6	ARI36332 Sequence
2	15	100.0	20	6	ARI44274 Sequence
3	13.4	89.3	20	6	ARI36346 Sequence
4	13.4	89.3	20	6	ARI44285 Sequence
5	13.4	89.3	20	6	ARI44300 Sequence
6	12	80.0	27	6	AX118436 Sequence
7	11.8	78.7	28	6	AR090369 Sequence
8	11.8	78.7	34	6	AR085821 Sequence
9	11.8	78.7	37	6	AR000592 Sequence
10	11.8	78.7	37	6	AR000593 Sequence
11	11.8	78.7	48	6	AR085815 Sequence
12	11.8	78.7	48	6	AR099164 Sequence
13	11.4	76.0	21	6	AR058934 Sequence
14	11.4	76.0	21	6	168720 Sequence
15	11.4	76.0	24	6	AR019297 Sequence
16	11.4	76.0	24	6	AR061841 Sequence
17	11.4	76.0	24	6	AR079365 Sequence
18	11.4	76.0	24	6	ARI47552 Sequence
19	11.4	76.0	24	6	134711 Sequence
20	11.4	76.0	24	6	167965 Sequence
21	11.4	76.0	39	6	AX080330 Sequence
22	11	73.3	22	6	ARI06133 Sequence
23	10.8	72.0	18	6	AI6427 synthetic
24	10.8	72.0	20	6	ARI36347 Sequence
25	10.8	72.0	20	6	ARI44286 Sequence
26	10.8	72.0	20	6	ARI44301 Sequence
27	10.8	72.0	21	6	ARI48681 Sequence
28	10.8	72.0	22	6	AR085274 Sequence
29	10.8	72.0	22	6	AR085275 Sequence
30	10.8	72.0	22	6	117705 Sequence
31	10.8	72.0	22	6	138617 Sequence
32	10.8	72.0	22	6	138618 Sequence
33	10.8	72.0	22	6	169338 Sequence
34	10.8	72.0	22	6	AX042926 Sequence
35	10.8	72.0	25	6	AX042926 Sequence
36	10.8	72.0	25	6	E13467
37	10.8	72.0	25	9	HUMXPA10A
38	10.8	72.0	27	6	AX012391
39	10.8	72.0	27	6	E59997
40	10.8	72.0	29	6	AX099585
41	10.8	72.0	29	6	137195 Sequence
42	10.8	72.0	31	6	137196 Sequence
43	10.8	72.0	31	6	137197 Sequence
44	10.8	72.0	31	6	137198 Sequence
45	10.8	72.0	31	6	137198 Sequence

ALIGNMENTS

RESULT 1  
ARI36332  
LOCUS ARI36332 20 bp DNA  
DEFINITION Sequence 135 from patent US 6136603.  
ACCESSION ARI36332  
VERSION ARI36332.1 GI:14477004  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.  
TITLE Antisense modulation of interleukin-5 signal transduction  
JOURNAL Patent: US 6136603-A 135 24-OCT-2000;  
FEATURES  
source location/Qualifiers  
1..20  
/organism="unknown"  
BASE COUNT 5 a 7 c 3 g 5 t  
ORIGIN

Parents

Query Match 100.0%; Score 15; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 TCTACCAAGACTTC 20

## RESULT 2

ARI44274 20 bp DNA PAT 08-AUG-2001  
LOCUS ARI44274  
DEFINITION Sequence 2 from patent US 6210892.  
ACCESSION ARI44274  
VERSION ARI44274.1 GI:15106141  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank, Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,  
Monia,B.P., Freier,S.M., McKay,R. and Karras,J.G.  
TITLE Alteration of cellular behavior by antisense modulation of mRNA  
processing  
JOURNAL Patent: US 6210892-A 2 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 5 a 7 c 3 g 5 t  
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 TCTACCAAGACTTC 20

## RESULT 3

ARI36346 20 bp DNA PAT 16-JUN-2001  
LOCUS ARI36346  
DEFINITION Sequence 149 from patent US 6136603.  
ACCESSION ARI36346  
VERSION ARI36346.1 GI:14477018  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.  
TITLE Antisense modulation of interleukin-5 signal transduction  
JOURNAL Patent: US 6136603-A 149 24-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 5 a 6 c 3 g 6 t  
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 TCTATCAAGACTTC 20

## RESULT 4

ARI44285 20 bp DNA PAT 08-AUG-2001  
LOCUS ARI44285  
DEFINITION Sequence 13 from patent US 6210892.  
ACCESSION ARI44285  
VERSION ARI44285.1 GI:15106152  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank, Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,  
Monia,B.P., Freier,S.M., McKay,R. and Karras,J.G.  
TITLE Alteration of cellular behavior by antisense modulation of mRNA  
processing  
JOURNAL Patent: US 6210892-A 13 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 5 a 6 c 3 g 6 t  
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 TCTATCAAGACTTC 20

## RESULT 5

ARI44300 20 bp DNA PAT 08-AUG-2001  
LOCUS ARI44300  
DEFINITION Sequence 28 from patent US 6210892.  
ACCESSION ARI44300  
VERSION ARI44300.1 GI:15106167  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank, Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,  
Monia,B.P., Freier,S.M., McKay,R. and Karras,J.G.  
TITLE Alteration of cellular behavior by antisense modulation of mRNA  
processing  
JOURNAL Patent: US 6210892-A 28 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 5 a 6 c 3 g 6 t  
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 TCTATCAAGACTTC 20

## RESULT 6

AXI18436 27 bp DNA PAT 11-MAY-2001  
LOCUS AXI18436/c  
DEFINITION Sequence 3559 from Patent WO0129262.  
ACCESSION AXI18436  
VERSION AXI18436.1 GI:14035387  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequence.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Picolult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 3559 26-APR-2001;  
Orchid Biosciences, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..27  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer"  
misc\_feature 1..27  
/note="n - C3 linker"  
BASE COUNT 5 a 5 c 7 g 9 t 1 others  
ORIGIN

Query Match 80.0%; Score 12; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.3e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ctaccaagactc 13  
Db 15 CTACCAAGGACT 4

RESULT 7  
AR090369/C  
LOCUS AR090369 28 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 489 from patent US 5994076.  
ACCESSION AR090369  
VERSION AR090369.1 GI:10017124  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Chenchik,A., Jekhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 489 30-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..28  
/organism="unknown"  
BASE COUNT 5 a 5 c 8 g 10 t  
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 28;  
Best Local Similarity 86.7%; Pred. No. 3.1e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15  
Db 21 TCTACCAAGGACATC 7

RESULT 8  
AR085821/C  
LOCUS AR085821 34 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 16 from patent US 5985281.  
ACCESSION AR085821  
VERSION AR085821.1 GI:10012587  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Taylorson,C.John, Eggelte,H.Johannes, Tarragona-Fiol,A.,  
Rabin,B.Robert, Boyle,F.Thomas, Hennam,J.Frederick,  
Blakey,D.Charles, Marsham,P.Robert, Heaton,D.William, Davies,D.Huw,  
Slater,A.Michael and Hennequin,L.FrancoisAndre.  
TITLE Chemical compounds  
JOURNAL Patent: US 5985281-A 16 16-NOV-1999;  
FEATURES Location/Qualifiers

source 1..34  
/organism="unknown"  
BASE COUNT 10 a 6 c 9 g 9 t  
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 34;  
Best Local Similarity 86.7%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15  
Db 19 TCTACCTAGGAATTC 5

RESULT 9  
AR000592  
LOCUS AR000592 37 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 24 from patent US 5736524.  
ACCESSION AR000592  
VERSION AR000592.1 GI:3963123  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)  
AUTHORS Content,J., Huygen,K., Liu,M.A., Montgomery,D. and Ulmer,J.  
TITLE Polynucleotide tuberculosis vaccine  
JOURNAL Patent: US 5736524-A 24 07-APR-1998;  
FEATURES Location/Qualifiers  
source 1..37  
/organism="unknown"  
BASE COUNT 5 a 12 c 13 g 7 t  
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 37;  
Best Local Similarity 86.7%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15  
Db 7 TCTACCATGGGCTTC 21

RESULT 10  
AR000593  
LOCUS AR000593 37 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 25 from patent US 5736524.  
ACCESSION AR000593  
VERSION AR000593.1 GI:3963124  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)  
AUTHORS Content,J., Huygen,K., Liu,M.A., Montgomery,D. and Ulmer,J.  
TITLE Polynucleotide tuberculosis vaccine  
JOURNAL Patent: US 5736524-A 25 07-APR-1998;  
FEATURES Location/Qualifiers  
source 1..37  
/organism="unknown"  
BASE COUNT 6 a 11 c 10 g 10 t  
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 37;  
Best Local Similarity 86.7%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15  
Db 7 TCTACCATGGGCTTC 21

RESULT 11  
LOCUS AR085815/c 48 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 10 from patent US 5985281.  
ACCESSION AR085815  
VERSION AR085815.1 GI:10012581  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Taylorson,C.John, Eggelte,H.Johannes, Tarragona-Fiol,A.,  
Rabin,B.Robert, Boyle,F.Thomas, Hennam,J.Frederick,  
Blakey,D.Charles, Marsham,P.Robert, Heaton,D.William, Davies,D.Huw,  
Slater,A.Michael and Hennequin,L.FrancoisAndre.  
TITLE Chemical compounds  
JOURNAL Patent: US 5985281-A 10 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..48  
BASE COUNT 15 a 10 c 13 g 10 t  
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 48;  
Best Local Similarity 86.7%; Pred. No. 2.9e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15  
Db 19 TCTACCTAGGAAATTG 5

RESULT 12  
LOCUS AR099164 48 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 47 from patent US 6077692.  
ACCESSION AR099164  
VERSION AR099164.1 GI:12808930  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Ruben,S.M., Jimenez,P., Duan,D.Roxanne, Rampy,M.A., Mendrick,D.,  
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.  
and Gentz,R.L.  
TITLE Keratinocyte growth factor-2  
JOURNAL Patent: US 6077692-A 47 20-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..48  
BASE COUNT 12 a 12 c 9 g 15 t  
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 48;  
Best Local Similarity 86.7%; Pred. No. 2.9e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15  
Db 25 TTTACCAAGTACTTC 39

RESULT 13  
LOCUS AR058934/c 21 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5837839.  
ACCESSION AR058934  
VERSION AR058934.1 GI:5984511

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Toth,M.John and Huwyler,L.Robin.  
TITLE DNA coding sequences for mevalonate Pyrophosphate decarboxylase  
JOURNAL Patent: US 5837839-A 5 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..21  
BASE COUNT 4 a 4 c 6 g 7 t  
ORIGIN

Query Match 76.0%; Score 11.4; DB 6; Length 21;  
Best Local Similarity 92.3%; Pred. No. 5.8e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 taccaggacttc 15  
Db 17 TAGCAAGCACTTC 5

RESULT 14  
LOCUS 168720 21 bp DNA PAT 04-FEB-1998  
DEFINITION Sequence 22 from patent US 5677141.  
ACCESSION 168720  
VERSION 168720.1 GI:2830842  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Isogai,T., Fukagawa,M., Iwami,M., Aramori,I. and Kojo,H.  
TITLE Process for producing 7-aminocephem compound or salts thereof  
JOURNAL Patent: US 5677141-A 22 14-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..21  
BASE COUNT 5 a 6 c 7 g 3 t  
ORIGIN

Query Match 76.0%; Score 11.4; DB 6; Length 21;  
Best Local Similarity 92.3%; Pred. No. 5.8e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 taccaggacttc 15  
Db 9 TACCACGACGCTC 21

RESULT 15  
LOCUS AR019297 24 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 3 from patent US 5783406.  
ACCESSION AR019297  
VERSION AR019297.1 GI:3974411  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Schumm,J.W. and Puers,C.  
TITLE Allelic ladders for short tandem repeat loci  
JOURNAL Patent: US 5783406-A 3 21-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..24  
BASE COUNT 7 a 7 c 6 g 4 t  
ORIGIN

Query Match 76.0%; Score 11.4; DB 6; Length 24;  
Best Local Similarity 92.3%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctaccaaggact 13  
||| |||||  
Db 9 TCTGCCCAAGGACT 21

Search completed: December 21, 2001, 11:34:02  
Job time: 16649 sec

Wed Dec 26 11:51:12 2001

us-09-800-629a-209.szlm50.rni

Page 1

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:39:11 ; Search time 303.16 Seconds  
(without alignments)  
11.206 Million cell updates/sec

Title: US-09-800-629A-209  
Perfect score: 15  
Sequence: 1 tctaccaagacttc 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/lna/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/lna/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/lna/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/lna/Backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	20	3	US-09-280-799-135
2	15	100.0	20	4	US-09-277-020-2
3	13.4	89.3	20	3	US-09-280-799-149
4	13.4	89.3	20	4	US-09-277-020-13
5	13.4	89.3	20	4	US-09-277-020-28
6	11.8	78.7	28	2	US-08-859-998-489
7	11.8	78.7	34	2	US-08-860-882A-16
8	11.8	78.7	37	1	US-08-338-992B-25
9	11.8	78.7	37	1	US-08-338-992B-25
10	11.8	78.7	48	2	US-08-860-882A-10
11	11.8	78.7	48	3	US-09-023-082A-47
12	11.4	76.0	21	1	US-08-314-309A-22
13	11.4	76.0	21	2	US-08-733-825-5
14	11.4	76.0	24	1	US-08-219-633-3
15	11.4	76.0	24	1	US-08-515-236-3
16	11.4	76.0	24	1	US-08-761-950-3
17	11.4	76.0	24	2	US-08-632-575B-33
18	11.4	76.0	24	2	US-08-687-080-156
19	11.4	76.0	24	3	US-08-933-358-12
20	11.4	76.0	24	4	US-09-327-229-5
21	11.4	76.0	24	5	PCT-US95-12608-5
22	11.4	76.0	39	3	US-08-444-644-4
23	11.4	76.0	39	3	US-09-120-365-58
24	11.4	76.0	22	4	US-09-515-039-58
25	10.8	72.0	20	3	US-09-357-070-26
26	10.8	72.0	20	3	US-09-280-799-150
27	10.8	72.0	20	4	US-09-277-020-14

28	10.8	72.0	20	4	US-09-277-020-29	Sequence 29, Appl
29	10.8	72.0	20	4	US-09-467-642-78	Sequence 78, Appl
30	10.8	72.0	21	4	US-09-262-773-38	Sequence 38, Appl
31	10.8	72.0	22	1	US-08-091-569-4	Sequence 4, Appl
32	10.8	72.0	22	1	US-08-091-569-5	Sequence 5, Appl
33	10.8	72.0	22	1	US-08-203-676-4	Sequence 4, Appl
34	10.8	72.0	22	1	US-08-203-676-5	Sequence 5, Appl
35	10.8	72.0	22	1	US-08-295-676A-10	Sequence 10, Appl
36	10.8	72.0	22	2	US-08-948-591-10	Sequence 10, Appl
37	10.8	72.0	22	2	US-08-822-238-4	Sequence 4, Appl
38	10.8	72.0	22	2	US-08-822-238-5	Sequence 5, Appl
39	10.8	72.0	23	3	US-09-120-887-8	Sequence 8, Appl
40	10.8	72.0	31	1	US-08-390-850-208	Sequence 208, App
41	10.8	72.0	31	1	US-08-390-850-209	Sequence 209, App
42	10.8	72.0	31	1	US-08-390-850-210	Sequence 210, App
43	10.8	72.0	31	1	US-08-390-850-211	Sequence 211, App
44	10.8	72.0	31	1	US-08-435-634-208	Sequence 208, App
45	10.8	72.0	31	1	US-08-435-634-209	Sequence 209, App

#### ALIGNMENTS

RESULT 1  
US-09-280-799-135 Application US/09280799  
Sequence 135, Appl  
Patent No. 6136603  
GENERAL INFORMATION:  
APPLICANT: Deap, Nicholas M.  
APPLICANT: Karris, James G.  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
FILE REFERENCE: ISPH-0340  
CURRENT APPLICATION NUMBER: US/09/280,799  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 135  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-280-799-135

Query Match 100.0%; Score 15; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccaagacttc 15  
Db 6 tctaccaagacttc 20

RESULT 2  
US-09-277-020-2  
Sequence 2, Application US/09277020  
Patent No. 6210892  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation  
FILE REFERENCE: ISPH-0339  
CURRENT APPLICATION NUMBER: US/09/277,020  
CURRENT FILING DATE: 1999-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 20

deem + have  
previously to present

Interfered  
GWS



TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-09-277-020-2

Query Match 100.0%; Score 15; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 tctaccaagacttc 20

RESULT 3

US-09-280-799-149  
Sequence 149, Application US/09280799  
Patent No. 6136603  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Karas, James G  
APPLICANT: McKay, Robert  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
FILE REFERENCE: ISPH-0340  
CURRENT APPLICATION NUMBER: US/09/280,799  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 149  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-09-280-799-149

Query Match 89.3%; Score 13.4; DB 3; Length 20;  
Best Local Similarity 93.3%; Pred. No. 29;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccabgacttc 15  
|||||  
Db 6 tctatcaagacttc 20

RESULT 4

US-09-277-020-13  
Sequence 13, Application US/09277020  
Patent No. 6210892  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation  
TITLE OF INVENTION: of mRNA Processing  
FILE REFERENCE: ISPH-0339  
CURRENT APPLICATION NUMBER: US/09/277,020  
CURRENT FILING DATE: 1999-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-09-277-020-13

Query Match 89.3%; Score 13.4; DB 4; Length 20;  
Best Local Similarity 93.3%; Pred. No. 29;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 tctatcaagacttc 20

RESULT 5

US-09-277-020-28  
Sequence 28, Application US/09277020  
Patent No. 6210892  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation  
TITLE OF INVENTION: of mRNA Processing  
FILE REFERENCE: ISPH-0339  
CURRENT APPLICATION NUMBER: US/09/277,020  
CURRENT FILING DATE: 1999-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-09-277-020-28

Query Match 89.3%; Score 13.4; DB 4; Length 20;  
Best Local Similarity 93.3%; Pred. No. 29;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
|||||  
Db 6 tctatcaagacttc 20

RESULT 6

US-08-859-998-489/c  
Sequence 489, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Jekhadze, George  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: .435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 489:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-489

Query Match 78.7%; Score 11.8; DB 2; Length 28;  
Best Local Similarity 86.7%; Pred. No. 2.6e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15  
||||| ||||| ||  
DB 21 TCTACCAGGACATC 7

RESULT 7  
US-08-860-882A-16/c  
Sequence 16, Application US/08860882A  
Patent No. 5985281  
GENERAL INFORMATION:  
APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
APPLICANT: TARRAGONA-FIOL, ANTONIO  
APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HUM  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 bases  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
US-08-860-882A-16

Query Match 78.7%; Score 11.8; DB 2; Length 34;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15  
||||| ||||| ||  
DB 19 TCTACTAGGAATTC 5

RESULT 8  
US-08-338-992B-24  
Sequence 24, Application US/08338992B  
Patent No. 5736524

GENERAL INFORMATION:  
APPLICANT: CONTENT, JEAN  
APPLICANT: HUYGEN, KRIS  
APPLICANT: LIU, MARGARET A.  
APPLICANT: MONTGOMERY, DONNA  
APPLICANT: ULMER, JEFFREY  
TITLE OF INVENTION: A POLYNUCLEOTIDE TUBERCULOSIS VACCINE  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,992B  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: YABLONSKY, MICHAEL D.  
REGISTRATION NUMBER: 40,407  
REFERENCE/DOCKET NUMBER: 19342  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-4678  
TELEFAX: 908-594-4720

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-338-992B-24

Query Match 78.7%; Score 11.8; DB 1; Length 37;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15  
||||| ||||| ||  
DB 7 TCTACCATGGCCTTC 21

RESULT 9  
US-08-338-992B-25  
Sequence 25, Application US/08338992B  
Patent No. 5736524  
GENERAL INFORMATION:  
APPLICANT: CONTENT, JEAN

APPLICANT: HUYGEN, KRIS  
APPLICANT: LIU, MARGARET A.  
APPLICANT: MONTGOMERY, DONNA  
APPLICANT: ULMER, JEFFREY  
TITLE OF INVENTION: A POLYNUCLEOTIDE TUBERCULOSIS VACCINE  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,992B  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: YABLONSKY, MICHAEL D.  
REGISTRATION NUMBER: 40,407  
REFERENCE/DOCKET NUMBER: 19342  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-4678  
TELEFAX: 908-594-4720  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-338-992B-25

Query Match 78.7%; Score 11.8; DB 1; Length 37;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
Db 7 TCTACCATGGCTTC 21

RESULT 10  
US-08-860-882A-10/c  
Sequence 10, Application US/08860882A  
Patent No. 5985281  
GENERAL INFORMATION:  
APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
APPLICANT: TARRAGONA-FIOL, ANTONIO  
APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HUW  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-10

Query Match 78.7%; Score 11.8; DB 2; Length 48;  
Best Local Similarity 86.7%; Pred. No. 2.8e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15  
Db 19 TCTACCTAGCAATTC 5

RESULT 11  
US-09-023-082A-47  
Sequence 47, Application US/09023082A  
Patent No. 6077692  
GENERAL INFORMATION:  
APPLICANT: RUBEN, STEVEN M.  
APPLICANT: JIMENEZ, PABLO  
APPLICANT: DUAN, D. ROXANNE  
APPLICANT: RAMPY, MARK A.  
APPLICANT: MENDRICK, DONNA  
APPLICANT: ZHANG, JUN  
APPLICANT: NI, JIAN  
APPLICANT: MOORE, PAUL A.  
APPLICANT: COLEMAN, TIMOTHY A.  
APPLICANT: GRUBER, JOACHIM R.  
APPLICANT: DILLON, PATRICK J.  
APPLICANT: GENTZ, REINER L.  
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,082A  
FILING DATE: 13-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01790  
FILING DATE: 14-FEB-1995  
PRIOR APPLICATION DATA:



MOLECULE TYPE: other nucleic acid  
US-08-733-825-5

Query Match 76.0%; Score 11.4; DB 2; Length 21;  
Best Local Similarity 92.3%; Pred. No. 4.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ttaccaaggacttc 15  
||| ||||| |||||  
Db 17 TAGCAAGACTTC 5

## RESULT 14

US-08-219-633-3  
Sequence 3, Application US/08219633  
Patent No. 5599666

## GENERAL INFORMATION:

APPLICANT: Schumm, James W.  
APPLICANT: Puers, Christoph  
TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT  
TITLE OF INVENTION: LOCI  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ross & Stevens, S.C.  
STREET: One South Pinckney Street, P.O. Box 2599  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53701-2599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/219,633  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 257-5353  
TELEFAX: (608) 257-9175  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-219-633-3

Query Match 76.0%; Score 11.4; DB 1; Length 24;  
Best Local Similarity 92.3%; Pred. No. 4.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttaccaaggact 13  
||| ||||| |||||  
Db 9 TCTGCCAAGACT 21

## RESULT 15

US-08-515-236-3  
Sequence 3, Application US/08515236  
Patent No. 5674686

## GENERAL INFORMATION:

APPLICANT: Schumm, James W.  
APPLICANT: Puers, Christoph  
TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT  
TITLE OF INVENTION: LOCI

NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ross & Stevens, S.C.  
STREET: One South Pinckney Street, P.O. Box 2599  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53701-2599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/515,236  
FILING DATE: 15-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/219,633  
FILING DATE: 28-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 257-5353  
TELEFAX: (608) 257-9175  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-515-236-3

Query Match 76.0%; Score 11.4; DB 1; Length 24;  
Best Local Similarity 92.3%; Pred. No. 4.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Search completed: December 21, 2001, 11:39:11  
Job time: 10842 sec

